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(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

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## Fields of the Invention

The present invention relates to purified single-stranded DNA molecules, purified single-stranded DNA molecules complementary thereto or purified double-stranded DNA molecules consisting of said single-stranded DNA molecules, which can specifically hybridize to human genomic DNA, human cDNA or human mRNA at particular sites. The DNA molecules of the present invention can be used for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting and diagnosing cellular abnormalities due to disease and viral infection, or distinguishing and identifying the cell type, and efficiently cloning genes expressed in a tissue-specific manner. The present invention further includes cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products or the like.

## Related Arts

Recognizing the importance of the most fundamental attribute of mRNA, that is, "the nature of the cell is determined by the expression pattern of genes as reflected in the population of mRNA", the inventors of the present invention have proposed "body mapping" as a unique approach to their objective. This is an entirely novel attempt to prepare "the information on gene expression" for presumably about 200 different kinds of cells and tissues present in the human body and elucidate when, where and to what extent a certain gene is expressed, and map genes to the respective organ or cell type in which they are expressed.

While a variety of cells in the living body express various proteins depending on their respective biological functions, the intracellular concentrations of these proteins vary according to the cell type, stage of development and differentiation, environment, etc.

In general, genes are classified into "genes encoding proteins essential for the life of the cell" and "genes encoding proteins responsible for functions specific to the cell". Of these two, "genes encoding proteins essential for the life of the cell" are expressed constantly in all types of cells and also called "housekeeping genes", while "genes encoding proteins responsible for functions specific to the cell" are often expressed specifically in a particular type of cells or a particular group of cells, and also may be specifically expressed at a particular stage of cellular development and differentiation. Furthermore, they are often "inducible genes" and the amount of their expression varies depending upon the environment to which cells are exposed. In other words, cells may grow as a result of the expression of "genes encoding proteins essential for the life of the cell" and display their specific functions as a result of the expression of "genes encoding proteins responsible for functions specific to the cell".

However, under abnormal cellular conditions due to disease or infection, the expression of genes within individual cells is altered as compared with that under the normal conditions. Especially, during viral infection, RNAs encoding virus-specific proteins are synthesized in large amounts within the cell, leading to the production of said protein in large amounts. In other words, the alteration in the expression level of genes within the cell, especially as reflected in the concentration of intracellular mRNA, can lead to such abnormal cellular conditions as seen in diseases.

Thus, the function of each cell in the living body is closely related to the expression status of genes within the cell. Accordingly, in order to elucidate the function of each cell at molecular level or to investigate the pathogenesis of a disease at molecular level, it becomes necessary to comprehend the expression status of cellular genes, especially the intracellular concentration of each mRNA.

A theoretically possible approach to this objective is the extraction and analysis of all cellular proteins for determination of expression status. However, although it may be possible to isolate a specific protein, in most cases it is almost impossible to completely isolate all of these proteins, because a great variety of proteins are expressed within the cell.

Another approach is to directly estimate the concentrations of cellular mRNAs corresponding to all intracellular proteins. However, although it may be possible to isolate a specific mRNA, it is practically impossible to completely isolate all of these mRNAs and directly estimate their amounts, because a great variety of mRNAs are synthesized simultaneously within the cell and furthermore they may be unstable and susceptible to enzymatic degradation during their extraction.

This invention aims to provide DNA molecules which can be used as probes or primers required for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting or diagnosing cellular abnormalities due to disease or virus infection, recognizing and identifying various cell types, and efficiently cloning genes expressed in a tissue-specific manner. Moreover, the present invention aims to provide cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products.

## Summary of the invention

In general, the genetic information flows in order from DNA to mRNA and to protein (F. H. C. Crick, 1958). That is, "the information for the amino acid sequence of a protein" is first transcribed into mRNA and then translated into protein.

To explain this in further detail mammalian genes commonly comprise a region encoding a protein and a region regulating the expression of said gene. The regions of a gene encoding protein (called "exons") are often separated by intervening sequences (called "introns"). When a gene is transcribed into RNA, the introns of the precursor RNA (pre-mRNA) are excised and exons are connected in tandem to form a contiguous structure coding for a particular protein (this process is called "splicing"). On the other hand, the region regulating the expression of gene comprises, in addition to the regions directly regulating transcription such as a promoter and operator which are present upstream of the transcription region, untranslated regions are located both upstream (5') and downstream (3') of the coding region. In particular, 3' untranslated region (3' UTR) is important for regulating expression, since it contributes to the transport and stability of mRNA. During the processing of pre-mRNA, a methylated cap is added at its 5' end, the 3' untranslated region is cleaved at a specific site, a poly(A) tail is attached by adding 100 - 200 adenylate residues to the cleaved end, and the coding regions are spliced together to form mRNA. The protein is then synthesized after attachment of ribosomes to the mRNA.

The inventors of the present invention have elucidated that, in general, when the intracellular level of a particular mRNA is high, the expressed amount of the corresponding protein is also elevated, and also that it is possible to estimate the relative concentration of each intracellular protein by estimating relative intracellular concentration of the corresponding mRNA [DNA sequence 2, 137-144 (1991); Nature genetics, 2, 173-179 (1992)].

Basically in the present invention, mRNA is extracted from a particular cell and cDNA is synthesized by conventional methods using reverse transcriptase. However, in the present invention, cDNA is synthesized using a method developed by the inventors of the present invention so as to reflect the relative intracellular concentration of mRNA. A cDNA library is constructed and a group of cDNAs representing the population of total mRNA are cloned and sequenced.

An approach which appears to be similar to the one used by the inventors of the present invention but is entirely different, is the method of cloning of a cDNA library constructed by the random priming by Venter et al.

Venter's group randomly cloned cDNAs from commercially available cDNA libraries derived from brain cells (catalog No. 936206, 936205 or 935, Stratagene, California) and determined their base sequences [Science 252, 1651-1656 (1991); Nature 355, 632-634 (1992)].

While the method used by Venter et al. involves sequencing of cDNAs obtained by random priming, this method has the following drawbacks:

- 1) Since random cloning of various regions of a single-stranded mRNA may often lead to the formation of many cDNA fragments without any mutual overlapping portions, it is difficult to determine whether these cDNA fragments are derived from the same mRNA or a different one,
- 2) The longer a mRNA strand, the higher the chance for said mRNA to be reverse-transcribed into cDNA, and
- 3) Since the availability of each primer to be used among random primers differs depending on their base sequences, the relative frequency of cDNA synthesis is variable.

From aforementioned reasons, the relative frequency of appearance of cDNA does not reflect the relative concentration of cellular mRNA. Consequently, it is impossible to determine the relative concentration of each mRNA and the actual population of intracellular proteins by using the method of Venter et al.

However, with the method developed by the inventor of the present invention, it is possible to construct a cDNA library which precisely reflects the relative concentration of mRNA without any of the aforementioned complications. Since, in the present invention, cDNA is synthesized using only "poly-T" as the primer, the 3' ends of the cDNA have "a poly A tail". Therefore, the synthesis of cDNA with "poly-T" as the sole primer is initiated from the 3' end resulting in the formation of 3'-oriented cDNA. Since the 3' untranslated sequence is unique to a particular mRNA species and not present in other mRNA species [Birnstiel, M. L., et al., Cell 41, 349-359 (1985)], almost all the 3' end-oriented cDNAs hybridize with specific mRNAs. Digestion of the resulting cDNA with a restriction enzyme MboI which recognizes the specific four-base sequence GATC results in the formation of cDNA extending from the 3'-terminus to the first MboI restriction site. In the present invention, each cDNA thus cloned and included in "a cDNA library faithfully reflecting the relative intracellular concentration of mRNA" is called a "gene signature" (abbreviated as GS hereinafter). A GS includes not only the double-stranded DNA but also each single-stranded DNA thereof.

The present invention relates to a purified single-stranded DNA, purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under the sequence identification number (SEQ ID NO) 1 - 7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA. The present invention also relates to a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1 - 7837 ( wherein T is read as U ) or any portion thereof at its 3' region and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA.

The present invention is explained further in detail as follows.

The DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1 - 7837 but also includes a single-stranded DNA containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

Furthermore, the DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any of the base sequences listed under SEQ ID NO 1- 7837 (wherein T is read as U) or any portion thereof at its 3' region but also includes a single-stranded DNA (or a single-stranded DNA complementary thereto) containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

In addition, the DNA of the present invention not only includes a single-stranded DNA or a single-stranded DNA complementary thereto but also includes a double-stranded DNA consisting of said single strands.

Obviously, the term "contain" as used herein does not necessarily mean that the DNA of the present invention contains at a single site without interruption (1) "a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1-7837 or a portion thereof" or (2) "a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any or any portion of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) at its 3' region or a portion of said single-stranded DNA." In other words, the term "contain" is applicable also to the case where one or more exogenous bases are inserted in the base sequence of the DNA (1) or (2).

The hybridization to a particular site of human genomic DNA, human cDNA or human mRNA can be achieved under standard conditions (see e.g., Molecular Cloning: A Laboratory Manual, Sambrook, J., et al., Cold Spring Harbor Laboratory Press, 1989). In the following preferred embodiment, there will be described methods for constructing a cDNA library which reflects precisely the relative intracellular concentration of mRNA, cloning cDNA groups which correspond to total mRNA, and determining the base sequence of each cDNA.

First, cells from specific tissues, for example, cells from organs, for example, cells derived from human liver (HepG2) are grown, and the total mRNA is extracted by standard procedures. mRNA thus obtained is attached to a vector to construct a cDNA library.

For example, mRNA is attached to the vector plasmid pUC19, which has the M13 sequences flanking the cloning site, as follows.

pUC19 is cleaved by HincII and PstI and poly-T of 20 bp - 30 bp is added to the PstI-digested end to which the 3'-end poly-A tail of the mRNA is hybridized (Fig. 1a). After the DNA strand is extended with conventional methods using reverse transcriptase, a double stranded DNA is formed with DNA polymerase (Fig. 1b). The double stranded DNA thus obtained is cleaved with the restriction enzyme MboI which recognizes a specific four base sequence (Fig. 1c).

MboI, which recognizes a four base sequence (GATC), cleaves the DNA within a few hundred bases from the poly-A tail. Since MboI is found to digest, without exception, about 300 human cDNAs which were randomly selected from the GenBank data base by the inventor of the present invention, this enzyme cleaves the cDNA to be cloned at a specific site. In addition, as pUC19 is prepared in dam<sup>+</sup> E. coli, e.g., E. coli JM109 and since its adenine at the MboI recognition site is methylated (G<sup>m</sup>ATC), it is not cleaved by MboI.



Subsequently, in order to prepare a vector containing the double-stranded DNA which has previously been attached to pUC19 and has the MboI-cleaved end, the pUC19 DNA is digested with BamHI to make termini cohesive with the MboI-cleaved end. Since the recognition sequence of BamHI (GGATCC) contains that of MboI (GATC), the extended portion of the double-stranded DNA is not cleaved with BamHI.

- 5 The resulting double-stranded DNA is then circularized by standard ligation methods, and the recombinant vector plasmid thus prepared is introduced into *E. coli*, e.g., *E. coli* DH5 in order to make a cDNA library.

With this method, only a clone containing the base sequence upstream of the poly-A tail of the mRNA is obtained.

- 10 Since the average size of the inserted cDNA fragment is relatively small, 270 bp, it is free from biased cloning resulting from variations in the efficiency of cDNA synthesis and transformation that occur in the case of larger sized DNAs. Furthermore, because instability due to repeated base sequences and the like is eliminated, the cDNA library of the present invention faithfully represents the relative concentration of mRNA in the cell.

- 15 Furthermore, when the cDNA inserted into the vector is relatively short, it is possible to accurately amplify the cDNA fragment using the sequence of the vector flanking it as a primer. It is also possible to determine the base sequence from the 5' end directly by the PCR without interference from the 3' poly-A tail which will reduce the accuracy of sequence determination.

Amplification of the GS, i.e., the cDNA fragment inserted into the vector, is performed as follows.

- 20 The *E. coli* cells in which the cDNA library is introduced are grown using standard methods and lysed. Debris contained in the bacterial lysate are removed by centrifugation and the supernatant containing the vector DNA is recovered. The vector DNA thus obtained is used as the DNA template for amplification by the PCR (Fig. 1d, amplification with PCR primers 1 and 2).

- 25 Base sequences flanking both ends of the GS is properly selected for use as primers and the PCR is performed under standard conditions. PCR products thus obtained are subjected to the elongation reaction using fluorescence primers complementary to the vector sequence flanking the 5' end of the GS, and the sequence is determined with an autosequencer (Fig. 1d, sequence determination with dye primer).

Based on the results of the sequence determination of each GS, the species and the frequency of appearance of the GS in each tissue or cell type are analyzed.

- 30 As to each cell type not only normal cells but also cells under pathogenic conditions (such as tumor cells, virus infected cells, etc.) can be used without any restriction. For example, liver cells (from fetus, neonate or adult), various hematopoietic cells (granulocytic, monocytic, etc.), lung cells, adipocytes, endothelial cells, osteoblasts, colon mucosa cells, retinal cells and hepatoma cells (HepG2, etc.), and promyelocytic leukemia cells (HL60, etc.) will be used. The appearance frequency for each GS is described for each cell type in Tables 1 through 219. There, patent number represents "SEQ ID NO for each GS", size represents the "length of each GS", and F represents the "sum of appearance frequencies in the cells studied". In addition, hepG2 stands for "hepG2 (a liver cancer cell line)", HL60 stands for "HL60 promyelocytic leukemia cell line", granulo stands for "granulocytoid, HL60 stimulated by DMSO", mono stands for "monocytoids, HL60 stimulated by TPA", 40 w liver stands for "40 w neonatal liver", 19 w liver stands for "liver of a 19 weeks old fetus, adult liver is "adult liver ", lung stands for "adult lung", adipose stands for "subcutaneous adipose tissue", endothel stands for "primary cultured aortic endothelium", osteoblast stands for "primary cultured osteoblast", colon mucosa is "colon mucosa", small cell carci stands for "small cell carcinoma of lung", retina is "retina", cerebral cortex is "cerebral cortex", adenocarci (lung) stands for "adenocarcinoma of lung", squamous cell ca (lung) stands for "squamous cell carcinoma of lung", keratinocyte stands for "primary cultured keratinocyte", fibroblast stands for "primary cultured fibroblast", Alzheimer stands for "Alzheimer temporal lobe", cerebellum stands for "cerebellum", visceral fat is "visceral fat", corneal epithelium is "corneal epithelium", peripheral granulocyte is "peripheral granulocyte", neuroblastoma is "neuroblastoma" and taste bud of tongue is "taste bud of tongue".

- 45 "Accession number of target mRNA" represents the accession number of the entry in GenBank Release 79 whose base sequence has homology with that of each GS, "match %" represents the percent homology of the GS sequence relative to that of said homologous sequence, "match starts at (GS)" represents the base position counted from the 5'-end of the GS at which the region for homology calculation starts, "match starts at (GenBank)" represents the base position counted from the 5'-end of the GenBank sequence at which the region for homology calculation starts, and "GenBank target size" represents the whole length of the GenBank sequence corresponding to the GS. The columns in Tables 1 - 219 represent the same items as in Table 1.

Based on the data in Tables 1 - 219, each GS can be classified into several groups. A GS, which is expressed at high frequency in a specific cell or groups of cells with similar property, for example,

promyelocytic leukemia cell, granulocyte and monocyte and not expressed entirely or expressed very little in other cells (groups), is a likely GS corresponding to the gene encoding "the protein responsible for functions specific to the cell" (e.g., GS0001553, GS0002047, GS004895, etc.). On the other hand, a GS, which is expressed commonly in every kind of cell, most likely corresponds to the gene encoding "the protein essential for the life of the cell" (e.g., GS0000019, GS0000155, GS000861, etc.). In addition, some GSs are expressed at low frequency (e.g., GS0000013, GS0002399, GS0003155, etc.).

Since the GS with the sequence determined as described above will reflect the population of mRNA expressed in a particular cell, it must be possible to find the relative concentration of mRNA in each cell by determining the appearance frequency for each GS in a cDNA library derived from that cell. Therefore, to confirm the correlation between the appearance frequency for each GS in a cDNA library and the relative concentration of cellular mRNA, the GS thus obtained was labeled with <sup>32</sup>P by standard methods and used as the probe in the following hybridization test. mRNA isolated from a specific cell is hybridized to said <sup>32</sup>P-labeled probe under standard conditions. The results of this Northern hybridization test were such that, when a GS found with high appearance frequency in a cDNA library was used as a probe, a dense band was formed, confirming the correlation of the frequency of appearance of the GS with the relative concentration of mRNA in the cell (see Example 5).

Similarly, the colony hybridization test of the cDNA library constructed as described above with a <sup>32</sup>P-labeled probe prepared as described above showed a close correlation between the frequency of appearance of the GS and the number of colonies hybridized with said GS (see Example 6), confirming the correspondence of the frequency of appearance of the GS and relative concentration of the GS in a cDNA library.

From the above results, by determining the appearance frequency of each GS in a cDNA library derived from a variety of cells, it has become possible to determine the expression status of the gene (or mRNA) corresponding to each GS. This fact implies conversely that each GS may be useful for industrial purposes as a specific probe or primer encoding information about the expression status of its corresponding gene (or mRNA) for each cell. For example, when it is proven that "a certain GS appears at high frequency only in a cDNA library derived from tissue A, that is, the gene corresponding to said GS is specifically expressed only in tissue A", by conventional cloning of the corresponding full-length cDNA using said GS as a probe or primer, it is possible to clone a full-length gene which is expressed in a tissue-specific manner.

Furthermore, for example, when it is proven that "the frequency of appearance of a certain GS is low in a cDNA library derived from tissue B, that is, the appearance frequency of the gene corresponding to said GS is low in tissue B", by examining the expression frequency of the gene corresponding to said GS in a test sample of tissue B from a patient using said GS as a probe or primer, it may be possible to identify the pathogenic gene, wherein an unusually high expression frequency of said gene being a strong indication that said GS may be the gene involved in the pathogenesis. Furthermore, by conventional methods for cloning said full-length cDNA using said GS as a probe or primer, it is possible to isolate said pathogenic gene and elucidate its characteristics.

In practice, the DNA of the present invention may be used as a probe or primer for detecting and diagnosing disease, cloning a pathogenic gene or related gene, cloning a viral gene, identifying and recognizing cell types, cloning a species-specific promoter and gene mapping.

One GS corresponds to one mRNA. It is therefore obvious that any portion of cDNA complementary to each mRNA carry the same "information for expression" as the GS. Accordingly, the DNA of the present invention is not restricted to "the DNA comprising the GS itself or portion thereof", but also includes the DNA comprising, for example, "a full-length cDNA complementary to each mRNA" and "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". They can be used as a probe or primer comprising the same "expression information" as that of the GS and can be used as a probe or primer in a similar manner as a GS. For example, by using a GS or a portion thereof as a probe or primer, it is obviously possible for those skilled in the art to readily isolate "a full-length cDNA corresponding to each mRNA" or "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". For example, as described hereinafter, conventional techniques such as "5' RACE", "nesting" and "inverse PCR" can be used.

An example of the method for detecting disease using the GS of the present invention will be described. As shown in Tables 1 - 219, with the method described above it is possible to detect a GS present specifically in a cDNA library constructed from each tissue by detecting and comparing the frequency of appearance of GS in each tissue. It is also possible to identify a GS corresponding to a protein which is expressed commonly in various tissues or which is expressed at low frequency. These GSs are denatured and then fixed on an appropriate filter, for example, nylon filter or nitrocellulose filter. It is

convenient to use a single filter with many GSs fixed on it. Usage of a single filter on which many denatured DNAs are fixed is well known. An example may be "the Escherichia coli Gene Mapping Membrane" (Takarashuzo, code No. 9035). It is a single nylon filter on which the cosmid contigs of genomic DNA of E. coli are fixed. It is possible to prepare a filter comprising a group of specific GSs corresponding to proteins expressed in a particular tissue, a filter comprising a group of GSs corresponding to proteins commonly expressed in various tissues, or a filter comprising a group of GSs corresponding to proteins expressed at low frequency. The single-stranded GSs fixed on these filters are then hybridized to labeled complementary DNA fragments synthesized using "random primers" prepared from template mRNA extracted from a test tissue, using four labeled nucleotides and reverse transcriptase (labeled mRNA can also be hybridized to the filters). Similarly, labeled complementary fragments synthesized using mRNA extracted from normal tissue as the template are hybridized (labeled mRNA can also be hybridized to the filters). If the profile of hybridization to a group of GSs has been categorized beforehand by comparing the hybridization profile of various pathogenic tissues to that of corresponding normal tissues, it is possible to diagnose the pathogenic condition of a particular test tissue by comparing the hybridization profile of the test tissue with that of the corresponding normal tissue and assigning that profile to a certain category. Virus infection can be detected in the same manner as in the case of other diseases.

Next, an example of the method for cloning pathogenic genes or their related genes using the GS of the present invention is described. As described above, using the filter on which denatured GSs are fixed, the GS-hybridization profile of various pathogenic tissues and that of corresponding normal tissues are compared. A considerable difference in the hybridization intensity between normal and pathogenic tissues will be an indication that the particular GS corresponds to a pathogenic gene. If a filter comprising only GSs specific for a particular tissue is applied to a sample from that particular tissue, the probability for detecting the GS with a great difference in hybridization intensity is elevated. Also a filter comprising GSs corresponding to proteins whose expression is low will facilitate the identification of the GS corresponding to the pathogenic gene by detecting an intense signal, because the hybridization signal for these GSs is usually weak. Once a GS corresponding to a pathogenic gene is found, said pathogenic gene can be cloned by established methods such as genomic Southern hybridization using said GS as a probe and/or a primer.

Furthermore, a method for cloning a full-length gene using a GS as a probe or primer is described in detail. Cloned genes isolated in the present invention are also appropriate for use in the production of proteins useful as pharmaceutical products. mRNA is extracted from tissues by conventional methods and cDNA libraries are then prepared (See Molecular Cloning, 2nd ed. Vol. 2, Section 8 New York; Cold Spring Harbor Laboratory). In this case, it is desirable to extract mRNA from tissues in which the target gene is highly expressed. One method to detect a specific gene in libraries thus prepared is, for example, to select positive clones via hybridization using a whole or partial GS as a probe. In general, since a GS is specific for a particular mRNA, hybridization can be carried out under certain stringent conditions. Probes used are at least more than 25 bases long, preferably more than 50 bases long, and more preferably more than 100 bases long.

Furthermore, if cDNA libraries, in which the cDNA for a specific gene is concentrated, are prepared, they will be preferable for selecting said specific gene. One method useful for this purpose is carried out as follows: 1) preparation of an affinity chromatographic column of resin on which the denatured GS corresponding to the specific gene is fixed; 2) application of mRNA extracted from a tissue to said column and retention of the mRNA species corresponding to the specific gene on said column; 3) elution and concentration of said retained mRNA; and finally 4) preparation of cDNA libraries using said concentrated mRNA species as the template. Another method is the selective amplification of cDNA corresponding to the specific gene by the PCR. Selective amplification of a specific gene is carried out as follows: using a partial sequence of a GS localized toward the 3' end of the specific gene as primer, cDNA is synthesized from mRNA with reverse transcriptase and 4 NTPs. To the 3' end of a single-stranded cDNA thus obtained a homopolymer such as poly-T is attached by the action of "terminal deoxynucleotidyl transferase (TdT)". In addition, using "a primer complementary to the homopolymer" and "a primer used in said reverse transcriptase reaction, or a primer whose sequence is included in the same GS but is located proximal to the 5' end", cDNA corresponding to the specific gene may be selectively amplified by the PCR [see 5'RACE (5' Rapid Amplification of cDNA ends): PNAS, Vol. 85, pp. 8998 - 9002 (1988); Nucleic Acids Res., Vol. 17, pp. 2919-2932 (1989)]. In addition, instead of the attachment of a homopolymer, there is another method comprising the following steps: 1) a single stranded anchor DNA is linked to the 3' end of a single stranded cDNA using "T4 DNA ligase"; and 2) said cDNA is amplified by the PCR using a primer complementary to said anchor DNA [Nucleic Acids Res., Vol. 19, pp. 5227-5232 (1991)]. Said primer is desirably more than 13 bases long, preferably more than 15 bases long, and more preferably more than 18

bases long. Furthermore, in order to enhance the efficiency of heat denaturation in the cycling reaction, said primer is preferably less than 50 bases long and more preferably less than 30 bases long. By linking said amplified DNA to a vector, a cDNA library concentrated with respect to the target gene is prepared.

In addition, it may be also possible to isolate a cDNA clone corresponding to the specific gene directly from the PCR products. Specifically, the PCR products are first separated by gel electrophoresis, subjected to Southern blotting analysis using the denatured GS as a probe, and examined for the presence of a band which specifically hybridizes to said GS. If a GS-hybridized band is detected, it is highly possible to isolate the cDNA clone corresponding to the specific gene by excising said band from the gel and subjecting it to direct cloning.

As described above, in order to further amplify the specific gene previously amplified by the PCR, it may be possible to perform the second PCR of the primary PCR products by replacing either or both primers previously used with a primer having the base sequence internal to said two primers (nesting) (Journal of Virology, Vol. 64, p. 864 (1990)). Nesting may be performed directly upon the products of the primary PCR. Alternatively, if a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of the primary PCR products, nesting may be performed for the DNA obtained by excision of the band followed by extraction. In the case where a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of nested products using the denatured GS as a probe, it is highly possible to successfully isolate the cDNA clone corresponding to the target gene by excising said band from the gel and subjecting it to direct cloning.

The isolated cDNA clone corresponding to the target gene may often correspond to the full-length mRNA, but it may be a cDNA with the 5' end deleted. In the case where the 5' end is deleted it is possible to isolate the full-length cDNA clone by conventional methods. For example, by screening a cDNA library using a probe comprising the base sequence in the 5' end region of the cloned cDNA, since the target position of said probe is shifted further toward the 5' end of the full-length cDNA than in the case of using a GS as a probe, it is possible to isolate only longer cDNA clones as the positive clone. Also by synthesizing cDNA using "a primer comprising the base sequence in the 5' end region of the cloned cDNA" with mRNA as the template followed by PCR amplification of "a single stranded cDNA having a homopolymer or anchor DNA sequence at the 5' end" and using "the primer used for previous cDNA synthesis or a primer having the sequence internal to that of said primer" and "a homopolymer or a primer complementary to anchor primer" as described above for the 5' RACE method, only the sequence toward the 5' side of the cDNA may be selectively amplified since the position of said primer is shifted further toward the 5' side of the full-length cDNA. Even if the cDNA thus obtained has a deletion at the 5' end, the population of cDNA fragments covering the full-length of the long cDNA may be obtained by repeating this procedure. It may be easy for those skilled in the art to obtain a full-length cDNA by suitably linking said cDNA fragments having overlap segments together.

Alternatively, by performing the inverse PCR (Inverse PCR: Genetics, Vol. 120, p. 621 (1988); Molecular Cloning, 2nd ed., Vol. 2, 14.12-14.13 (New York; Cold Spring Harbor Laboratory)), it may be possible to isolate a cDNA clone extending externally from the GS, that is, in the genomic DNA region. Specifically, the target DNA (genomic DNA or cDNA) is digested with restriction enzymes into fragments of about 2-3 kb and then circularized by ligating the cleaved ends. By performing the PCR for said DNA using "a set of primers which are complementary to the cDNA clone isolated using the GS or the GS as a probe or primer, and thereby making the direction of DNA synthesis mutually opposite (outward), it may be possible to amplify the DNA region extending externally from the GS. There is known a method to isolate a full-length genomic DNA of a specific gene by repeating this procedure (Nucleic Acids Res., Vol. 16, p. 8186 (1988)).

In addition, although "Taq polymerase" is conventionally used in the PCR described above, the cloning procedure may be more efficiently performed using the "LAPCR (long and accurate PCR) technique (Nature Genet., Vol. 7, p. 350-351 (1994), Nature., Vol.369, p.684-685(1994)).

Furthermore, needless to say that by linking said full-length gene thus obtained to a suitable expression vector followed by its expression in an appropriate host, it is possible to obtain the corresponding gene product (Molecular Cloning, 2nd ed.).

Next, there will be described an example of the method for identifying and recognizing cell types using the GS of the present invention. As shown in Tables 1 - 219, based on the appearance frequency of GS in each tissue and its comparison among tissues, it is possible to identify those GSs specifically present in a cDNA library constructed for each tissue. These "tissue-specific GSs" are fixed on a filter. It will be more convenient if GSs specific to each tissue are collected and fixed on a filter as a whole (e.g., a GS block specific for hepatocytes or cerebral cortex cells). As described above, to this filter are hybridized labeled complementary fragments synthesized using "random primers" prepared from mRNA extracted from test tissues or cells, "nucleotide containing 4 labeled nucleotides", and "reverse transcriptase". (Directly labeled

mRNA can also be hybridized to the filters.) Depending on the type of tissues or cells, intense hybridization signals will be observed with the GS groups specific to said tissue or cell. Furthermore, a tissue-specific promoter can be cloned by structure analysis of the 5' upstream sequence through the cloning of the corresponding gene using established methods such as genomic Southern hybridization with the "tissue-specific GS" as the probe and/or primer.

These tissue-specific promoters thus obtained are useful for gene therapy in the future.

Gene therapy in a narrow sense aims to supplement the defective protein of patients using gene technology, and in this case it is necessary to express the exogenous gene in a desired tissue in a desired quantity. For this purpose, a promoter which is known to be expressed in a specific tissue in a desired quantity (in most cases a large quantity is desired) is highly useful. Although, at present, a virus promoter is often used, it can be inactivated by endogenous modification such as methylation. Promoters provided by tissue-specific GSs will be ideal substitutes for viral promoters.

There will be described the method for chromosomal assignment of DNA corresponding to the GS of the present invention using the probe derived from the GS obtained as described above.

First, the Southern blotting method will be described.

According to this method, for example, chromosomes are isolated from a lymphoblast cell line of human normal karyotype (e.g., GM0130b), and then a monochromosomal hybrid cell is prepared by introducing each human chromosome into non-human cells, such as rodent cells, and cultured on a large scale by standard methods. Then the DNAs extracted from said hybrid cells are digested with various restriction enzymes and subjected to agarose gel electrophoresis. Then, the electrophoresed DNAs are hybridized to <sup>32</sup>P-labeled GS prepared as described above and used as the probe. By identifying the hybrid cell the DNA of which is hybridized to said probe, it is possible to identify the chromosome in which the DNA corresponding to the GS of the present invention is present. Southern hybridization test of the total human genomic DNA using each labeled GS as a probe formed a single band corresponding to the GS, indicating that the DNA of the present invention can be used as a desirable probe for human genomic DNA. It is obvious that a desirable probe for human genomic DNA can be used also as a desirable probe for human cDNA and human mRNA.

A method similarly using the PCR to determine chromosomal localization of the GS of the present invention will be described.

To prepare most appropriate primers, base sequences are selected from the sequence of the GS in question by conventional methods, for example, by using the computer software OLIGO4.0 (National Biosciences) and the oligonucleotides (20-24mer) having the selected sequences are synthesized. The preferred size of the sequence to be amplified by the PCR is from 50mer to 100mer.

Using the primers thus synthesized and the chromosomal DNA extracted from the monochromosomal hybrid cell as such as the template, amplification by the PCR is performed in a conventional manner. Resulting PCR products are subjected to non-denatured acrylamide gel electrophoresis and stained with ethidium bromide for fluorescent detection. The sizes of these PCR products are then determined.

Chromosomal assignment is confirmed when the presence of a PCR product of correct size is confirmed.

It is evident that a chromosome or chromosomes in which the DNA corresponding to a GS is localized can be identified by using these procedures. It has also become evident that the DNA of the present invention can be used as desirable primers for human genomic DNA since a single band has resulted from amplification of the total human genomic DNA by the PCR using primers designed based on each tested GS. Obviously, a desirable primer for human genomic DNA is also a desirable primer for human cDNA and human mRNA.

#### Brief Description of Figures

Fig. 1 shows the preparation of 3' Mbol cDNA library.

Fig. 2 shows the results of tests of primers. A shows the location of primers on the vector; and B shows the electrophoretic patterns of DNA fragments amplified using the primers (A). Primers used are as follows: lane 1, FW (-40)/RV (-14); lane 2, FW (-40)/RV (-36); lane 3, FW (-40)/RV (-71); lane 4: FW (-40)/RV (-29); and lane 5, FW (-47)/RV (-48). Artifacts are indicted by arrows.

Fig. 3 shows the electrophoretic pattern of PCR products using FW(-40) and RV(-14) as primers. The lane at the right end shows the electrophoretic pattern of size markers and the other lanes show the PCR products using FW (-40)/RV (-14) as primers.

Fig. 4 shows the mRNA concentration reflecting the frequency of appearance of each GS in the cDNA library: especially, Fig.s 4A - 4D; experimental results; Fig. 4E, photographs of colonies; and Fig. 4F,

summary.

Fig. 5 shows the appearance frequencies for various cDNAs in the 3'-directed HepG2 cDNA library.

Fig. 6 shows the genetic mapping of each GS (gs) using PCR.

Fig. 7 shows the genetic mapping of each GS (gs) using PCR.

5 Fig. 8 shows the genetic mapping of each GS (gs) using PCR.

Fig. 9 shows the genetic mapping of each GS (gs) using PCR.

Fig. 10 shows the genetic mapping of each GS (gs) using PCR.

Fig. 11 shows the chromosomal mapping of GS001418 (gs001418) using PCR.

Fig. 12 shows the chromosomal mapping of GS001457 (gs001457) using PCR.

10 Fig. 13 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 14 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 15 summarizes the characteristics of hybrid cells used for Southern hybridization.

Fig. 16 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000152 (clone s14g02) as a probe.

15 Fig. 17 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000041 (clone s650) as a probe.

Fig. 18 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000181 (clone hm01e01) as a probe.

20 Fig. 19 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000055 (clone c13a18) as a probe.

Fig. 20 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000180 (clone s479) as a probe.

Fig. 21 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000094 (clone s173) as a probe.

25 Fig. 22 shows Southern blotting of chromosomal DNA from the hybrid cells using junk (clone hm01g02) as a probe.

Fig. 23 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double cleavage with EcoRI and BamHI.

30 Fig. 24 shows the chromosomal mapping of each GS by Southern-blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 25 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 26 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

35 Preferred embodiments of the invention

In the following section, there will be explained preferred embodiments of the present invention. However, the present invention will not be restricted to these preferred embodiments.

40 [Example 1]

#### Preparation of mRNA

45 Cytoplasmic RNA was extracted from a liver cancer cell line HepG2 (Aden., et al., Nature 282, 615-617, 1979) using standard procedures [Sambrook, J., et al., Molecular Cloning, 2nd ed. (New York: Cold Spring Harbor Laboratory), vol. 1, pp. 7.3-7.36, 1989]. Briefly, HepG2 cells grown in Dulbecco's modified Eagle medium supplemented with 10% FCS were lysed in RNA extraction buffer [0.14 M NaCl, 1.5 mM MgCl<sub>2</sub>, 10 mM Tris-HCl (pH 8.6), 0.5% NP-40, 1 mM DTT, 1000 units/ml RNase inhibitor (Pharmacia)] by using a  
50 Vortex mixer for 30 sec and then left standing on ice for 5 min. Nuclei and other cell debris were precipitated by centrifuging at 12,000 g for 90 sec, and the supernatant was deproteinized with Proteinase K followed by phenol extraction. RNA was precipitated by isopropanol and rinsed with 70% ethanol. Finally, the poly A<sup>+</sup> fraction was collected by oligo dT column fractionation (Aviv., et al., Proc. Natl. Acad. Sci. USA 69, 1408-1412, 1972).

55

## [Example 2]

## Preparation of vector primer DNA and construction of cDNA libraries

5 To prepare a vector primer, pUC19 DNA amplified in JM109 cells (Yanisch-Perron, C., et al., *Gene* **33**, 103-119, 1985) was digested with PstI to completion and a poly T-tail was added with terminal transferase (Pharmacia) to a mean length of 26. This process was monitored by the incorporation of <sup>3</sup>H-deoxythymidine triphosphate [Okayama, H., et al., *Methods in Enzymology* (San Diego: Academic Press), vol. **154**, pp. 3-28, 1987]. The product was digested by HincII, and the resulting short fragments were eliminated by  
10 chromatography with Sepharose S-300. Then the T-tailed plasmid was purified by an oligo dA column and stored in 50% ethanol at a concentration of 1 µg/µl.

Fig. 1 shows the outline of the construction of the cDNA library. Two micrograms each of the cytoplasmic Poly A<sup>+</sup> RNA and the vector primer DNA were co-precipitated in 70% ethanol containing 0.3 M Na-acetate and the pellet was dissolved in 12 µl of distilled water. For the first strand synthesis, after heat  
15 denaturation at 76°C for 10 min, 4 µl of 5 x reaction buffer [250 mM Tris-HCl (pH 8.3), 375 mM KCl, 15 mM MgCl<sub>2</sub>], 2 µl of 0.1 M DTT and 1 µl of 10 mM each of dATP, dCTP, dGTP and dTTP were added to the sample at 37°C. The reaction was initiated by the addition of 200 units of reverse transcriptase MMLV-H-RT (BRL), and after incubation at 37°C for 30 min, stopped by transferring the reaction tube onto ice. For the second strand synthesis, to the aforementioned reaction mixture the following was added: 92 µl of  
20 distilled water, 32 µl of 5 x E. coli reaction buffer [100 mM Tris-HCl (pH 7.5), 20 mM MgCl<sub>2</sub>, 50 mM (NH<sub>4</sub>)-<sub>2</sub>SO<sub>4</sub>, 500 mM KCl, 250 µg/ml of BSA, 750 µM βNAD], 3 µl of 10 mM each of dATP, dCTP, dGTP and dTTP, 15 units of E. coli ligase (Pharmacia), 40 units of E. coli polymerase (Pharmacia), and 1.5 units of E. Coli RNase H (Pharmacia). The reaction mixture was then incubated at 16°C for 2 h and heated to 65°C for 15 min. Then 20 units each of BamHI and MboI were added, and the reaction mixture was incubated at  
25 37°C for 1 h and heated again at 65°C for 30 min. Finally, the sample was diluted up to 1 ml with 1 x E. coli reaction buffer, and 100 units of E. coli ligase were added. The resulting mixture was incubated at 16°C overnight. An aliquot of this mixture was used to transform competent E. coli DH5 cells (Toyobo). Transformants were selected by ampicillin resistance. The product was named "3' MboI cDNA library".

## 30 [Example 3]

## Amplification of cDNA insert by PCR

The plasmid-carrier E. coli colonies were picked into 96-well plates containing 125 µl of LB medium  
35 (Davis, R. W., et al., *Advanced Bacterial Genetics*. New York: Cold Spring Harbor Laboratory, 1980) in each well and incubated in a moist chamber at 37°C for 24 h. A replica culture was made for every plate using a 96-pinned replica device (Sigma) and the master plates were stored at -80°C for future use. After overnight incubation at 37°C, 50 µl of the culture from each well of these replicas were transferred to polycarbonate 96-well plates (Techne). Bacteria were collected by centrifugation in an Omnispin H4211 rotor (Sorvall) at  
40 1500 rpm for 5 min, resuspended in 50 µl of water, covered with a layer of mineral oil and lysed at 95°C for 30 min in a metal bath. Debris were removed by centrifugation at 3600 rpm for 30 min in the same rotor.

Five microliters of the supernatant were added to 20 µl of distilled water and kept at 95°C for 10 min under a layer of mineral oil. Then the denatured lysate was subjected to PCR by adding 25 µl of 2 x reaction mixture [40 mM Tris-HCl (pH 8.9 at 23°C), 3 mM MgCl<sub>2</sub>, 50 mM KCl, 200 µg gelatin/ml]  
45 containing 5 pmol each of primers, 5 nmol each of dATP, dCTP, dGTP, dTTP and 1.25 units of Taq DNA polymerase (Cetus) at 70°C. Temperature cycling reactions were carried out immediately after addition of the reaction mixtures using a thermal cycler either for microfuge tubes (PJ1000, Perkin Elmer Cetus) or for a 96-well plate (PHC-3, Techne); 35 repeated cycles of 30 sec at 96°C, 1 min at 55°C, and 2 min at 72°C without a final extension step were performed.

50 For this method, the correct choice of primers for the PCR reaction is crucial. Therefore, preliminary tests were performed using the following primers with a predicted T<sub>m</sub> of above 60 °C.

The primers tested were a pair of primers, FW(-47) and RV(-48), which are identical to the commercially available 24 mer primers, a second pair of primers, [FW(-40) and RV(-29)], which are a longer version (21 mer) of the well-tested sequencing primers, and the primers RV(-71) and RV(-14), which have a triplet  
55 sequence at the 3' terminus identical with that in FW(-40) but is in the opposite orientation (Fig. 2A).

In most of the cases where various combinations of primers were tested, short PCR artifacts appeared, besides the expected major products (Fig. 2B, arrows indicate the PCR artifacts.). These artifacts could be reduced by raising the annealing temperature, lowering the primer concentration or lowering the substrate

concentration but in all cases the yield of the products was not high enough to serve as a template for the sequencing reaction without concentration thereof.

However, since one pair of primers [SW(-40) and RV(-14)] did not yield artifacts (Fig. 3), this pair was selected for further tests, and was found to give reproducible results. Similar results were obtained with randomly selected cDNA clones. Therefore, only this pair of primers SW(-40) and RV(-14) was used as the primers of the present embodiment.

[Example 4]

#### 10 DNA sequencing

The PCR products were drop-dialyzed against TE [10 mM Tris-HCl (pH 8.0), 1 mM EDTA] on millipore filter (VS 0.025  $\mu$ m) for 90 min while stirring. Forty-eight samples are easily applied on a single filter of 150 mm diameter. Without further purification the samples were subjected to the Cycle Sequencing protocol (Applied Biosystems, 1991) using dye labeled primers with minor modifications. For dideoxycytidine sequencing reaction, 2  $\mu$ l of the dialyzed PCR reaction product (about 0.2 pmol of template DNA) were added to 3  $\mu$ l of a reaction mixture containing 0.4 pmol of FAM M13 (-21) Primer (Applied Biosystems) in 160 mM Tris-HCl (pH 8.9), 40 mM  $(\text{NH}_4)_2\text{SO}_4$ , 10 mM  $\text{MgCl}_2$ , 50  $\mu$ M dATP, 12.5  $\mu$ M dCTP, 75  $\mu$ M 7-deaza-dGTP (Boehringer Mannheim Biochemicals), and 50  $\mu$ M dTTP, 25  $\mu$ M ddCTP, 0.8 unit of Taq Polymerase (Perkin Elmer Cetus), and subjected to 15 plus 15 cycles of the reaction (95 °C 30 sec, 60 °C 1 sec, 70 °C 1 min and 95 °C 30 sec, 70 °C 1 min) according to the manufacturer's recommendation in a 96-well plate using a thermal cycler (PHC-3, Techné). The three other sequencing reactions for dideoxyguanosine, dideoxyadenosine, and dideoxythymidine were performed in parallel (with TMRA, JOE, and ROX primers respectively, supplied by Applied Biosystems) in an identical fashion, except that twice the volume of all the ingredients was added to the dideoxyguanosine and dideoxythymidine reactions. Each sample, from a set of four was cooled to 4 °C, pooled, precipitated with ethanol, resuspended in 6  $\mu$ l of a solution of formamide/50 mM EDTA (5/1 by v/v), loaded onto sequencing gel and analyzed by a DNA autosequencer (Model 373A Ver 1.0.1, Applied Biosystems).

#### 30 [Example 5]

The frequency of appearance of each GS of the cDNA library reflects mRNA population.

To confirm that our 3'-directed regional cDNA library was a non-biased representation of the mRNA population in HepG2 cells, the inserts of four cDNA clones (EF-1 $\alpha$ ,  $\alpha$ 1-antitrypsin, hnRNP core protein A1 and inter- $\alpha$ -trypsin inhibitor) from the clones redundantly obtained by random selection of cDNA were radiolabeled and used as probes in a Northern analysis of poly A<sup>+</sup> mRNA from the HepG2 cells. (The results are shown in Fig. 4A-D, and summarized in Fig. 4F.) The relative band intensity of the four mRNA species demonstrated that their relative ratios were 52, 24, 1 and 1.2, respectively (lane iii in Fig. 4F). Then the same set of probes was used for measuring the number of colonies hybridizing with each probe in the same cDNA library of 8,800 clones (Fig. 4E).

The clonal frequencies were 307, 128, 7 and 9, or in ratio, 44, 17, 1 and 1.3, respectively (lane iv in Fig. 4F). These two estimates agreed, showing that the cDNA library used is a non-biased representation of the mRNA population. The ratio was practically unchanged when different preparations of mRNA from the same cell were tested.

Fig. 4 shows the proportionality of the composition of the 3'-directed cDNA library and of the mRNA. Fig. 4A, 2  $\mu$ g of poly A<sup>+</sup> RNA from HepG2 cells was electrophoresed in lanes 1-4 of a formamide agarose gel containing ethidium bromide (5  $\mu$ g/ml) and then exposed to UV. Lane 5 is the RNA ladder (BRL) used as size markers (kb). In Fig. 4B, the filter was northern blotted using the following <sup>32</sup>P-labeled 3'-specific cDNA probes: Elongation factor-1 $\alpha$  (lane 1),  $\alpha$ 1-antitrypsin (lane 2), hnRNP core protein A1 (lane 3), inter- $\alpha$ -trypsin inhibitor (lane 4). In Fig. 4C, one pmol each of the non-labeled cDNA fragments [EF-1 $\alpha$  (lane 1),  $\alpha$ 1-antitrypsin (lane 2), hnRNP core A1 (lane 3), inter- $\alpha$ -trypsin inhibitor (lane 4), were electrophoresed in a 2% agarose gel, then photographed. Fig. 4D is a Southern analysis of the blotted filter from Fig. 4C, using the same set of radioactive probes. Lane 5 shows the migration pattern of the reference 1 kb ladder (BRL). Hard copies of these screen images were taken at 8 h for b, and 1 h for d. The radioactivity in each band was counted directly in a scinti-scanner ( $\beta$ -603; Betagen) and registered in (i) and (ii) in Fig. 4F. The observed band intensities were corrected based on the band intensities in Fig. 4D (ii in Fig. 4F), and normalized relative to the value of probe 3 (hnRNP core A1, lane iii in Fig. 4F) as 1 (iii in Fig. 4F). These values represent the relative content of each mRNA species in the original mRNA preparation. Fig. 4E



shows the results of colony hybridization of the membranes carrying 8,800 colonies of the 3'-directed cDNA library using the same set of the four radioactive probes. Positive colonies were counted and registered (iv in Fig. 4F), then normalized with the value of HnRNP core protein A1 as 1. The numbers in B, D and E in Fig. 4 represent the probe No. in Fig. 4F. Fig. 4F shows a remarkable agreement between the values of lanes (iii) and (v).

#### [Example 6]

##### Population study of the cDNA library

To analyze further the composition of the cDNA library, 7 and 10 clones were selected from the redundant (group I) and solitary (group II) sequence groups, respectively, and these inserts were used as radiolabeled probes for colony hybridization (Fig. 6). The frequencies of the colonies that hybridized with group I probes were roughly identical to those that were randomly picked and sequenced. These frequencies were about 3.5%-0.1%. Nearly 52% of the cDNA library population consisted of the redundant sequence group containing 173 species. When 8 probes from group II were tested, 18 positive colonies were identified among 26,400 colonies screened, giving an average frequency of 0.007%. Two probes did not hybridize with any of the 26,400 colonies, resulting in the average frequency of <0.004%. Thus, the average frequency of the 10 probes in group II was several orders of magnitude less than the lowest of group I.

The results are summarized in Fig. 5, showing the appearance frequencies of various DNA species in the 3'-directed HepG2 cDNA library. In Fig. 5, seven cDNA probes (a15 through tb042) were selected from the 162 identified genes in the redundant group (group I), and ten (s155 through s632) were randomly chosen from the solitary group (group II). In columns A, B and C, each one of the insert DNAs was radiolabeled and used as a probe for colony hybridization tests of 982 (A), 8,800 (B) or 26,400 colonies (C). NT indicates "not tested". The DDBJ entry names of the 17 clones listed in this table are HUM000A15, HUM000C321, HUM000B038, HUM000M01B02, HUM000C13A04, HUM000M02D02, HUM000TB042, HUM000S155, HUM000S159, HUM000S639, HUM000S635, HUM000S170, HUM000S154, HUM000S167, HUM000S645, HUM000S647, and HUM000S632.

#### [Example 7]

##### Analyses of sequencing errors

All the sequence data presented in this specification were obtained by repeated cycles of enzymatic amplification of the plasmid inserts, followed by cycle sequencing with Taq polymerase. Sequences of 60 clones that showed data bank matches were examined for discrepancies from the data bank entries. It was found that the accuracy in the region 1-100 bp distant from the cloning site was 98.7%, indicating that the primers or probes designed with the sequence in this region could be obtained practically without any erroneous sequences or even if they contain any errors, they are functionally without problems.

#### [Example 8]

##### Mapping of GS by PCR

###### <cDNA sequence>

cDNA library was constructed from mRNA of DMSO treated HL60 cells. The methods for construction of the 3'-directed cDNA library and for sequence analysis of the library components are the same as described in Examples 1-4.

###### <PCR primer>

Primer design was performed by using the computer software OLIGO 4.0 (National Biosciences) which eliminates possible formation of inter- or intra-molecular secondary structures. In addition to the primer design, transfer of oligonucleotide sequences to the local database and synthesizer were semiautomated using a Macintosh computer linked with a network. DNA oligomers were synthesized on an automated DNA synthesizer (Model 394, Applied Biosystems) on a 40 nmol scale. The synthesized oligomers were used as

PCR primers without further purification.

(Preparation of Genomic DNA)

5 The human genomic DNA was extracted from the normal karyotype lymphoblastoid cell line GM0130b. Mouse and Chinese hamster genomic DNAs were purchased from Clontech. Monochromosomal hybrid cells utilized for mapping panel were commonly used ones which have been described previously. Briefly, chromosomes 3, 4, 9, 11, 12, 13, 15, 22 and Y were carried in human-Chinese hamster monochromosomal hybrid cells, and chromosomes 1, 2, 5, 6, 7, 8, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21 and X were carried  
10 in the human-mouse monochromosomal hybrid cells A9 series. The integrity of the hybrid cells were monitored by *in situ* hybridization.

(Amplification by Polymerase Chain Reaction)

15 PCR was performed according to standard protocols (Saiki, R. K., et al., Science 230, 1350-1354, 1985), using 10 pmol of each primer on a whole 20  $\mu$ l scale reaction, with 35 thermal cycles of 30 sec at 94 °C, 60 sec at an annealing temperature, and 90 sec at 72 °C, using a Perkin-Elmer 9600 thermal cycler. Annealing temperature was determined according to the "optional annealing temperature" estimated by the Program OLIGO.

20

(Analysis of the PCR Products)

The PCR products were run on an 8% polyacrylamide non-denatured gel (Acrylamide:Bis-acrylamide = 19:1, 1 mm thick) at 300 V for 1 h, followed by staining in 90 mM Tris-borate, 2 mM EDTA buffer solution containing 0.25  $\mu$ g/ml ethidium bromide for 15 min. The size of the amplification products were determined  
25 relative to the 10 bp DNA ladder (BRL). Detection of fluorescence was performed by using a laser fluorescent image analyzer (FM-BIO, Hitachi Software Engineering). The image data were transferred to a computer for analysis.

30 (Results of Analysis of the PCR Products)

Among various species of 3'-directed cDNA-GSs obtained from granulocytoid cells, 195 novel GSs which did not match the sequences deposited in Genbank Release 76 were selected and used for designing primers for the PCR. The PCR was performed with these primers using the total human genomic  
35 DNA as the template.

Among the 195 primer pairs, 191 (98%) yielded products whose size matched those expected within 5 nt. The results are summarized in Figs. 6 - 10 whose figure legends are as follows: GS, gene signature; CN, clone name; Chromosomal position, chromosome numbers to which GSs were mapped; Sequence of primers, DNA sequences of primers (Sense, sense strand; anti-sense, anti-sense strand); AT, annealing  
40 temperature; HO, Observed size of PCR products with total human genomic DNA (nt); HE, Expected size of PCR products with total human genomic DNA (nt); MO, Observed size of PCR products with mouse genomic DNA (nt); CO, Observed size of PCR products with Chinese hamster genomic DNA (nt); G, Number of "hits" of GS in the granulocytoid (DMSO treated HL60) cDNA library after analyzing altogether 1000 clones; T, Total number of "hits" of the GS after analyzing altogether 3000 clones from the three  
45 cDNA libraries of HL60 with and without induction by DMSO or TPA. Question marks ("??") indicate that the PCR products did not yield a clear band.

"M" indicates that the PCR products yielded a band which was indistinguishable from the band observed after the reaction using mouse DNA as the template. Similarly, "C" indicates that the PCR products yielded a band which was indistinguishable from the band after the reaction using Chinese  
50 hamster DNA as the template.

The overall rate of success of the PCR was 191/195 (98%), although GSs were randomly selected from the cDNA sequences, indicating that the quality of the cDNA library used in this work was reliable, and that the sequence analyses and primer designs were performed appropriately. Thus, the possible chances of failure of the PCR caused by presence of an intron(s) in the relevant cDNA sequences is negligible in  
55 working with the GS, as introns virtually do not lie in the poly A proximal 3'-region of vertebrate genes (Wilcox et al., Nucleic Acids Res. 19, 1837-1843, 1991). This is a big advantage compared to the use of partial fragmented cDNA sequences obtained from randomly primed cDNA libraries (Adams et al., Science 252, 1651-1656, 1991) or from 5'-directed cDNA libraries.

## (Chromosomal assignments of GS)

The 191 primer pairs that yielded PCR products from total human DNA were used for chromosomal assignments of the GSs with the monochromosomal hybrid cell panel. At least 119 GSs were assigned to a single chromosome. As an example, GS001418, shown in Fig. 11, was assigned to chromosome number 3. With some clones, extra products were obtained, some of which were assigned to the same chromosome, whereas others to different chromosomes. An example, GS001457, is shown in Fig. 12. Sixty-two (33%) clones yielded the expected PCR products with two or more different chromosomes. Thirty-five cases (18%) yielded PCR products whose size were indistinguishable from background rodent genomic DNA. Among these, 21 GSs produced products indistinguishable from mouse and Chinese hamster DNA. Ten GSs yielded no expected PCR products with the monochromosomal cell panel DNA although the expected PCR products from total human genomic DNA were observed. The 10 cases probably arose from a small deletion in the hybrid cells. Five clones obtained from HepG2 cDNA library have been analyzed also by Southern blot analysis. Four out of the 5 GSs (GS000053, GS000120, GS000271 and GS000279) gave consistent results with those obtained by the PCR. One GS (GS000228), which was uncertainly assigned to chromosome Y because of the weak signal detected by the Southern blot method, was assigned to chromosome 11 by PCR.

## [Example 9]

## Mapping of GS by Southern blot method

## (Cell lines)

Total human genomic DNA was isolated from the human normal karyotype lymphoblastoid cell line GM0130b. Monochromosomal hybrid cells used as the mapping panel are shown in Fig. 15. Hybrid A9(neo-x)-y cells as described by Koi, et al. (Jpn. J. Cancer Res. 80, 413-418, 1989) were donated by Dr. M. Oshimura, Faculty of Medicine, Tottori University, passaged 3 times and frozen for storage. The loss or rearrangements of chromosomes could have occurred during this period. The GM series was obtained from the Mutant Cell Repository, National Institute of General Medical Science (NIGMS) (Camden, NJ). To confirm that human chromosomes remained intact in the hybrid cells after storage in liquid nitrogen, metaphase spreads of the hybrid cells were monitored by chromosome staining based on *in situ* hybridization using biotinylated total human DNA as the probe (Durnam, D. M., et al., Somatic cell Mol. Genet. 11, 571-577, 1985). Intact, as well as translocated or fragmented human chromosomes were easily detected by this means. In a hybrid cell mapping panel, chromosomes 11, 12 and 15 were represented by the hybrid cell lines A9(neo-11)-1, A9(neo-12)-4 and A9(neo-15)-2, respectively, and in another panel, they were represented by the hybrid cell lines GM10927A, GM10868 and GM11418, respectively.

## (Isolation of genomic DNA and Southern blotting)

High molecular weight DNA was extracted from cells using sodium dodecyl sulfate (SDS) and Proteinase K, followed by phenol-chloroform extraction and ethanol precipitation. DNAs were digested overnight with a combination of two restriction enzymes including EcoRI, BamHI and BglII. About 5 µg of each digest was electrophoresed in an 0.8% agarose gel, then transferred to Hybond N<sup>+</sup> membrane (Amersham) with 0.4 N NaOH. The membrane was rinsed in 2 x SSC and stored at 4 °C for subsequent use.

Clones containing a novel sequence and having more than 150 bp were selected as probes. The cDNA inserts of the clones were amplified by the PCR. The PCR products were isolated by electrophoresis through a 2% low-melting temperature agarose gel (Nusieve : SeaPlaque, 3 : 1), followed by excision. The gel was removed by melting at 65 °C and digesting with β-Agarose I (Bio Labs) at 40 °C for 1 h. The probes were labeled with [ $\alpha$ -<sup>32</sup>P]dCTP by random priming using a commercial kit (Amersham). Hybridization proceeded at 65 °C in a high salt buffer containing 6xSSC, 1x Denhardt's solution and 0.5% SDS, in the presence of 0.1 mg/ml of sonicated, denatured salmon sperm DNA. The membranes were washed in 2xSSC, 0.1% SDS at 65 °C for 30 min, then twice for 30 min in 0.1xSSC, 0.1% SDS at 65 °C, and analyzed using a Fuji BAS-2000 imaging analyzer.

## (Analyses with Genomic DNA)

Among the HepG2 3'-directed cDNA libraries described in Examples 1 and 2, 160 novel clones were selected and used as probes for Southern blots.

5 Total human genomic DNA was isolated from a cell line GM0130b that has a normal karyotype, and digested with the restriction enzymes, EcoRI, BamHI and BglII alone or in combination. The GS clones used as probes were the 3'-directed cDNAs. Each of these cDNAs covers a region between the poly(A) site and the nearest MboI site (GATC) (Okubo, K., et al., Nature Genetics 2, 173-179, 1992) and thus do not have restriction sites for BamHI or BglII. In addition, because the average size of GS is 270 bp, the chances of  
10 having an EcoRI site in the cDNA moiety were not high. In fact, only 7 clones out of the 160 analyzed had an EcoRI restriction site.

Membranes blotted with digested human genomic DNA were hybridized with radio-labeled GS probes and washed at high stringency. Since the 3'-terminal region of cDNA has, in general, a unique sequence which differs from that of protein encoding regions which tend to have conserved motifs, cross hybridization  
15 with unrelated cDNA sequences will not occur under such stringency. Examples of the results of hybridization are shown in Figs. 13 and 14. Clones s503 and s632 (Figs. 13a and 13b; junk) respectively represent unique single band producers. As shown below, 67 clones belonged to this class. The positions of the GS sequence relative to the restriction sites were inferred from the band patterns. Clone s311 (Fig. 13c; GS000092) showed a single band with EcoRI -as well as (EcoRI + BamHI)-digested DNA, but two bands of  
20 different sizes in other double digests. The double digestion thus helped resolve multiple GSs. Similar results were obtained with clone c13a08 (Fig. 13d; GS000055), in which there were 2 bands with EcoRI- or (EcoRI + BamHI)-digested DNAs, and 4 when digested with (EcoRI + BglII) or (BamHI + BglII). On the other hand, 4 hybridization bands appeared with clone s479 with EcoRI alone, but the number of bands decreased with (EcoRI + BglII) and (BamHI + BglII) (Fig. 14e; GS000180). These results indicate that  
25 genomic DNAs should be digested in various ways to reveal the maximum number of hybridizing fragments. The results of the analysis showed that 41, 10, 7 and 19 clones contained 2, 3, 4 and 5 or more bands, respectively. Clones s14f01 and tw1-46 (Figs. 14f and 14g; GS000407 and junk, respectively) contained at least 10 bands in each lane. Since the EcoRI restriction site is not present in the two GS sequences, the multiplicity of bands is likely to represent the multiple copy number of these genes. Clone  
30 kmb07 moved as a smear (Fig. 14h; junk), even after intensive high stringency washes, suggesting that this probe has a repetitious sequence which has not been hitherto identified.

## (Chromosomal assignments)

35 A set of monochromosomal hybrid cells carrying a single human chromosome in a background of rodent chromosome was collected (Fig. 15). Thirteen cell lines were microcell hybrids established by Koi et al. (Koi, M., et al., Jpn. J. Cancer Res. 80, 413-418, 1989) and the others were obtained from NIGMS. The results of monitoring the human chromosomes in these cell lines by *in situ* hybridization using biotinylated total human DNA are also presented in Fig. 15.

40 The GSs were assigned to chromosomes using hybrid cell mapping panels. Three types of membranes were prepared, each having DNAs prepared from hybrid cells, and digested with EcoRI, (EcoRI + BamHI), or (BamHI + BglII). Among these three types of membranes, the one which should have yielded the maximum number of bands was used for each GS probe, according to the results of total genomic Southern blots. Examples of hybridization results are shown in Figs. 16 - 22. The numeral on each lane represents the  
45 human chromosome numbers which is contained in the hybrid cell, and H stands for the total human chromosomes. Clone s14g02 (GS000152; Fig. 16) that showed a single hybridization band with the total human DNA digested with EcoRI (lane H), showed the corresponding band only with the hybrid cell line containing human chromosome 4. Thus, this GS lies in chromosome 4.

The clone s650 (GS000041; Fig. 17) was assigned to chromosome 12 which showed a characteristic  
50 7.5kb band in the presence of an (EcoRI + BamHI)-digested membrane. However, with an EcoRI digested DNA, the clone could not be assigned, as the human-specific and the cross-reacting rodent DNA fragments overlapped. The single, but shorter fragment band (1.3kb) which appeared in lanes 3, 4, 9, 13 and 22 represents the homologous DNA sequence in Chinese hamster, and the 3.3kb band in other lanes represents the homologous DNA in the mouse.

55 Clone hm01e01 (GS000181; Fig. 18) exhibited two fragments when hybridized to total human DNA treated with EcoRI alone, and these corresponding bands appeared in lanes 1 and 2. Thus, the two members of this gene family are located on two chromosomes.

Fig. 19 shows that clone c13a08 (GS000055) exhibited 4 bands when hybridized to (BamHI + BglII)- or (EcoRI + BglII)-digested total human DNA, although only 2 bands appeared with EcoRI- or (EcoRI + BamHI)-digested human DNA. Therefore, the (BamHI + BglII)-digested DNA panel was used for this clone. Two bands (12.3kb and 7.5kb) appeared in lane 7, a 5.2kb band in lane 2, and a 3.2kb band in lane 17. Two bands (6.0kb and 3.8kb) that cross-reacted with Chinese hamster DNA appeared in lanes 3, 4, 9, 13 and 22, and a single band (3.5kb) that cross-reacted with mouse DNA appeared in other lanes.

Clone s479 (GS000180; Fig. 20) showed 4 EcoRI fragments with total human DNA. The hybridization to an EcoRI-digested DNA panel yielded in bands of 10.5kb in lanes 7 and 19, 8.5kb in lane 8, 7.8kb in lanes 11 and 12, and 3.5kb in lane 11. Thus, the human specific genes are dispersed among chromosomes 7, 8, 11, 12 and 19, among which the 10.5 and 7.8kb bands in the total DNA both consist of two overlapping fragments. As shown in lane H, the intensity of these overlapping fragments was higher than normal. The 3.5kb band in lane H, as well as in lane 11 was also intense, suggesting that it also represents overlapping fragments.

Clone s173 (GS000094) exhibited 5 bands in EcoRI-cleaved total DNA (Fig. 21). Four corresponding fragments included a 4.5kb fragment in lane 1. Another 4.5kb band was observed in lane 4, indicating that the corresponding band in lane H overlapped. In addition, an intense 3.1kb band was observed in lane 17.

Clone hm01g02 (junk; Fig. 22) exhibited many bands with total DNA, and with those from monochromosomal hybrids. This clone must represent a multiple and closely related family of genes. It also contains a sequence conserved in homologous rodent genes which also give rise to multiple bands. Since most of the human specific and rodent bands overlapped, the chromosomes could not be assigned. Other combinations of restriction enzymes did not resolve the overlap.

The results of the total genomic DNA analyses and the chromosome assignments of 160 GSs are summarized in Figs. 23 - 26. Through total genomic DNA analyses using 4 differently digested human DNAs, 67 clones were categorized into a single band group, 41 in a two band group, 10 in a three band group, 7 in a four band group and 19 in a group that yielded five or more bands. Nine clones did not show any hybridization band under fixed conditions.

Assignment of two band clones showed that the two genes lie in different chromosomes in 15 of them, whereas the gene represented by clone s317 originated from the same chromosome. The three band clones s308 (GS000412) and s401 (GS000224) showed that two of the fragments lie on the same chromosome, and clone hm05g02 (GS000209) and s17a10 (GS000294) showed bands in different chromosomes. Clones displaying four or more bands showed a relatively dispersed distribution among chromosomes. "junk" in Example 9 is the DNA segment cloned by the same method used for GS but is not numbered.

#### [Example 10 Cloning of gene using GS]

[10A. Cloning of a full length cDNA encoding a human ribosomal protein, homologue of yeast S28. Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(1)]

Using a primer (5'-TGAAATTTATTACTACAGTGTTCACCA-3' (SEQ ID NO:7839)) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00500 and a primer (5'-TAATACGACTCACTATAGGG-3' (SEQ ID NO: 7840)) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, HepG2 cDNA library was amplified by the PCR and a full length cDNA clone encoding a human ribosomal protein, a homologue of yeast ribosomal protein S28 was isolated. (Hori et al., Nucl. Acids Res. 21: 4394, 1993).

[10B. A human ribosomal protein homologous to rat L9 ribosomal protein-Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(2)]

Using a primer 5'-CTTCTTTCTGTAGCCAGGTAAGTCT-3' (SEQ ID NO: 7841) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00418 and a primer (SEQ ID NO: 7840) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, a full length cDNA clone encoding a human ribosomal protein homologous to rat L9 was isolated (Hori et al., Nucl. Acids Res. 21:4395, 1993).

[10C. A human protein homologous to bovine phosphatidylethanolamine-binding protein. Cloning of the full length cDNA by hybridization using a probe comprising a partial sequence of a GS]

By hybridization with the probe,

5' - GATCGTTCTTCATGGGGTAAGAAAAGCTGGTCTGGAGTTGCTGAATG

TTGCATTAATTGTCCTGTTTGCTTGTAGTTGAATAAAAATAGAAACCTGAAT

GAAGGAAA-3' (SEQ ID NO:7838),

that comprises a partial sequence of HUMGS00421, a full length cDNA clone encoding a human protein homologous to bovine phosphatidylethanolamine-binding protein was isolated (Hori et al., Gene 140:293, 1994).

[10D. Human mpl-ligand. Cloning of a cDNA coding for the human mpl-ligand using a GS]

This embodiment employs the 5' SLIC (single ligation to single stranded cDNA) method which is an improved version of the 5'RACE (rapid amplification of cDNA ends) method, and is described in Nucleic Acids Res., 19, 5227-5232 (1991).

#### ① Reverse transcription of cDNA and attachment of anchor

The template was prepared using the reagents of the 5'-Amplifinder™ Kit (Toyobo, Inc.) in accordance with the protocol included therewith. Specifically, 2μg of human fetal liver poly A<sup>+</sup>RNA (Clontech Laboratories, Inc.) and 10 pmol of the primer PA-6, a primer corresponding to the 3' end of the gene signature (GS) sequence HUMGS02342 and consisting of the sequence 5'-TTTTCGGCGCTCCCATTATTCCTT-3' (SEQ ID NO: 7842), were mixed together and then denatured by heating the mixture at 65°C for 5 min. The cDNA was synthesized by combining the denatured sample with AMW reverse transcriptase, RNase inhibitor, dNTPs, and a reaction buffer, and then heating the resultant mixture at 52°C for 30 min. EDTA was then added to the mixture to stop the reaction. Thereafter, the RNA was hydrolyzed by adding NaOH to the reaction mixture and heating the resultant mixture at 65°C for 30 min. The mixture was then neutralized with acetic acid. A suspension of glass beads (GENO-BIND™) and NaI were added to the neutralized solution and the cDNA was adsorbed onto the beads. The cDNA, adsorbed onto the beads, was washed with an aqueous solution of 80% EtOH, and then eluted in 50 μl of distilled water. Glycogen was added to the solution of purified cDNA, and the cDNA was precipitated with EtOH and resuspended in 6 μl of distilled water. The resultant suspension (2.5 μl) was added to a solution containing 4 pmol of AmpliFINDER Anchor (5'-CACGAATTCATCTCGATTCTGGAACCTTCAGAGG NH<sub>2</sub>-3') (SEQ ID NO: 7843) provided with the Kit, T4 RNA ligase, and a ligation (reaction) buffer. The reaction mixture was incubated at room temperature overnight, and the AmpliFINDER Anchor primer in the reaction mixture was thereby ligated to the 3' end of the cDNA. The ligated product was then used as a template for the subsequent PCR.

#### ② Amplification by PCR

The primary PCR was carried out using the template produced in the procedure described above (①), the Anchor primer, 5'-CTGGTTCGGCCACCTCTGAAGTTCCAGAATCGATAG-3' (SEQ ID NO: 7846) and the PA-5 primer consisting of the sequence 5'-CTCGCTCGCCCATCCTTATACAGGCTCAGTTTGTCT-3' (SEQ ID NO: 7844). Specifically, 1 μl of the template was mixed with Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-5 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 μl and the PCR was performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.). The reaction mixture was subjected to 40 cycles of the PCR, wherein each cycle consisted of incubating the sample in sequence at 94°C for 1 min, 63°C for 1 min, and 72°C for 3 min and, in the last PCR cycle, at 72°C for an additional 8 min. The products of the PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of

approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered using a Sephaglas Bandprep Kit™ (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the gel was dissolved in a solution of Nal and the resultant mixture was heated at 60 °C for 10 min. Sephaglas™ BP  
 5 was added to the gel mixture and the DNA was adsorbed onto the glass beads contained therein. The glass beads, containing the adsorbed DNA, were then washed three times with a Wash Buffer provided with the Kit and eluted in 30 µl of TE buffer (10 mM Tris-HCl pH 8.0, 1mM EDTA).

One µl of the eluted DNA was used as a template in a secondary PCR. In order to enhance the specificity of the secondary PCR, the reaction was performed with PA-4 primer which consisted of the  
 10 sequence 5'-CTCGCTCGCCCATGTATAGGGACAGCATTCTGAGAG-3' (SEQ ID NO: 7845) and was positioned within the template sequence internal to the PA-5 primer and the Anchor primer. Specifically, 1 µl of the template was mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-4 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 µl preheated at 94 °C for 6 min, and the  
 15 secondary PCR was then performed under the same conditions described above (①) for the primary PCR. The products of the secondary PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered and purified under the same conditions as described above (①) for the primary PCR.

### 20 ③ Subcloning into plasmid vector

The purified DNA product of the secondary PCR was subcloned into the plasmid vector pUC18 (pharmacia Corp.), using a SureClone™ Ligation Kit (Pharmacia Corp.) in accordance with the protocol  
 25 included therewith. Specifically, the purified DNA was added to a solution containing Klenow polymerase, polynucleotide kinase and a reaction buffer, mixed and heated at 37 °C for 30 min in order to create blunt-ended termini and to phosphorylate the 5' terminus of the DNA molecules contained in the reaction mixture. The blunt-ended and phosphorylated DNA was combined with a solution containing 50 ng of a dephosphorylated and Sma I-cleaved pUC18 vector provided with the Ligation Kit, T4 DNA ligase, DTT and a  
 30 ligation reaction buffer, and the resultant mixture was warmed at 16 °C for 3 hr. One sixth volume of the reaction solution was employed to transform E. coli competent cells using standard methods. Specifically frozen E. coli competent cells (Wako Pure Chemical Industries, Ltd.) were thawed and mixed with the ligated DNA. The resultant mixture was incubated on ice for 20 min, heat-treated at 42 °C for 45 sec, and then incubated on ice for 2 min. A medium [Hi-Competence Broth (Wako Pure Chemical Industries, Ltd.)]  
 35 was added to the mixture containing the transformed E. coli cells. The mixture was incubated for 37 °C for 1 hr and then spread onto agar plates containing 100 µg/ml Ampicillin, 40 µg/ml X-Gal (6-bromo-4-chloro-3-indolyl-β-D-galactoside), 0.1 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and cultured overnight at 37 °C. White colonies were selected from the colonies which consequently appeared on the agar plates and analyzed by the PCR to determine the presence or absence of the DNA insert. Specifically, a sample of a  
 40 selected colony was picked with a sterilized toothpick and used to inoculate a 50 µl reaction solution containing 1 unit of Taq DNA polymerase, dNTPs, PCR buffer, 200 µM each of the M13 P4-22 primer consisting of the sequence 5'-CCAGGGTTTCCAGTCACGAC-3' (SEQ ID No: 7847) and M13 P5-22 primer consisting of the sequence 5'-TCACACAGGAAACAGCTATGAC-3' (SEQ ID No: 7848), wherein both primers are comprised of sequences complementary to the pUC18 vector. The resultant mixture was  
 45 heated at 94 °C for 6 min and then subjected to 30 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence, at 94 °C for 1 min, 55 °C for 1 min, and 72 °C for 2 min. The amplified insert was detected by electrophoresis of the PCR products on an agarose gel and thereby the clone pR02342-2, containing an insert, was selected.

### 50 ④ Sequencing of cDNA

The plasmid DNA was prepared using the QIAprep-Spin Kit (Funakoshi, Ltd.) in accordance with the standard alkali-SDS protocol included therewith. Specifically, E. coli cells transformed with the DNA of clone  
 55 pR02342-2 were cultured overnight in Luria Broth medium containing 100 µg/ml Ampicillin. The cultured cells were then pelleted by centrifugation and resuspended in P1 solution provided in the Kit. The resultant cell suspension was mixed with the P2 alkali solution of the Kit, incubated at room temperature for 5 min, neutralized with N3 solution of the Kit, incubated on ice for an additional 5 min and then centrifuged. The supernatant obtained from the centrifuged solution was applied to a QIAprep-Spin column. The Spin column

was then washed in sequence with PB and then PE solution of the Kit and the DNA was eluted from the column with TE buffer. Sequencing of the eluted DNA was then carried out using the sequencing kit PRISM™ Terminator Mix (Applied Biosystem Corp). Approximately 1 µg of the purified DNA was mixed with a solution containing 3.3 pmol of either the M13 P4-22 primer or M13 P5-22 primer and 9.5 µl of PRISM™ Terminator Mix. The M13 P4-22 and M13 P5-22 primer were used to sequence both strands of the DNA insert of clone pR02342-2. The resultant mixture was diluted to a final volume of 20 µl with distilled water and subjected to 25 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence at 96 °C for 30 sec, 50 °C for 15 sec, and 60 °C for 4 min. The excess primers and fluorescent dye present in the reaction mixture were removed by gel filtration using a MicroSpin™ S-200 HR column (Pharmacia Corp.) and the DNA products of the sequencing reaction were precipitated with EtOH. The precipitated DNA was resuspended, sequenced using an automated sequencer, "Model 373A" (Applied Biosystem Corp.), and thereafter analyzed to determine the nucleotide sequence.

The analysis of the nucleotide sequence revealed that the insert of clone pR02342-2, including the PA-4 primer, was 608 bp in length. The sequence of this insert was subjected to a search for homologous sequences entered in the Gen Bank data base, and a 100% match was found to a sequence in the cDNA which encodes the human mpl-ligand (Accession No. L 33410, Nature 369, 533-538, 1994). Further comparison of the insert of clone pR02342-2 with the cDNA sequence of the human mpl-ligand revealed that the cloned insert contained 81 bp of the 3' coding region of open reading frame. In addition, the insert of clone pR02342-2 contained an additional sequence extending beyond the 3' end of the human mpl-ligand cDNA sequence registered under Gen Bank Accession No. L 33410. These findings suggest that, using the GS HUMGS02342, the inventors of the present invention succeeded in cloning a cDNA clone pR02342-2, which could possibly have a different and more desirable property for expression than the human mpl-ligand cDNA represented by the sequence registered under Gen Bank Accession No. L 33410.

#### 25 ⑤ Cloning of the full-length cDNA encoding the human mpl-ligand

In order to find an optimal PCR primer, an appropriate computer program is used to search the sequence downstream of the coding region of the human mpl-ligand (clone pR02342-2) and thereby a primer PA-7 is designed and synthesized. A PCR similar to that described above in ② is performed using the template produced by the procedure described above in ①, the Anchor primer, and the PA-7 primer. Specifically, 1 µl of the template is mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-7 primer and Anchor primer. The resultant reaction mixture is diluted with distilled water to a final volume of 50 µl and the PCR is performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.) under conditions similar to that described above in ②. The products of the PCR are then resolved by electrophoresis on a 1% agarose gel and a band greater than 1300 bp in length, representing a product of the PCR, is recovered and cloned into a suitable vector in a manner similar to that described in ③. The cloned DNA is sequenced in a manner similar to that described in ④. The sequence is then compared to that of the human mpl-ligand cDNA registered under Gen Bank Accession No. L 33410 to confirm the presence of the full-length open reading frame.

Alternatively, using the Takara La PCR Kit (Takara Shuzo Inc., Code No. RR011) in accordance with the protocol included therewith, performing the 5'RACE procedure using primers similar to those described above in ②, a cDNA of approximately 2 Kb in length, corresponding to the human mpl-ligand, was isolated.

The tables of appearance frequencies for all GSs related to the present invention are followed by "Sequence Listing" for these GSs, wherein HUMGS numbers after the heading 'clone' represent GS numbers. In the sequence table, N in the base sequence stands for "A or C or G or T or U". However, since nucleic acids in the Sequence Listing are DNAs, "T or U" stands for T in this case.

By the present invention, it has become possible to provide DNA molecules which carry "the information for expression" in various cells and can be used for detecting and diagnosing the cellular abnormalities, recognizing and identifying cells and further efficiently cloning genes which are expressed in a tissue-specific manner, and furthermore cloned DNA molecules which can be used for the production of proteins useful as pharmaceutical products.



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1	00001	00001	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2	00002	00002	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
3	00003	00003	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
4	00004	00004	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	00005	00005	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	00006	00006	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	00007	00007	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	00008	00008	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	00009	00009	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	00010	00010	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	00011	00011	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	00012	00012	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	00013	00013	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	00014	00014	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	00015	00015	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	00016	00016	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	00017	00017	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	00018	00018	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	00019	00019	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	00020	00020	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	00021	00021	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AN	MA	QA	CA	SA	LA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
22	00023	00021	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	00026	00022	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	00028	00023	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	00029	00024	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	00030	00025	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	00031	00026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	00033	00027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	00034	00028	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	00036	00029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	00037	00030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	00038	00031	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	00039	00032	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	00040	00033	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	00041	00034	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	00042	00035	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	00043	00036	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	00044	00037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	00045	00038	5	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	00046	00039	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	00047	00040	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	00048	00041	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	00049	00042	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	00050	00043	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	00051	00044	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	00053	00045	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	00055	00046	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	00056	00047	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	00057	00048	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	00060	00049	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	00061	00050	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	00062	00051	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	00064	00052	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	00065	00053	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	00066	00054	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	00067	00055	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	00068	00056	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 2

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK			
58	00069	00057	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M34664	92.4	344	1	1484	2202			
59	00070	00058	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
60	00071	00059	7	1	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
61	00072	00060	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
62	00073	00061	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M16961	93.4	376	1	1131	1538			
63	00074	00062	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
64	00075	00063	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
65	00076	00064	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
66	00077	00065	34	1	3	2	5	1	0	0	2	2	0	1	1	1	0	1	0	4	0	0	0	0	0	0	0	0	D23660	97.9	439	1	980	1418		
67	00078	00066	12	1	0	1	1	0	0	0	1	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	X07979	90.9	572	1	3054	3614		
68	00079	00067	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	U04953	94.4	533	1	3741	4508		
69	00080	00068	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L08246	93	415	4	3501	3934		
70	00081	00069	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X70218	91.6	250	1	837	1382		
71	00082	00070	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
72	00083	00071	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
73	00084	00072	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	K03195	99.3	410	1	2134	2856		
74	00085	00073	26	5	3	1	0	0	1	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M84334	94.6	406	1	1356	1760	
75	00086	00074	4	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
76	00087	00075	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
77	00088	00076	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
78	00089	00077	33	1	3	2	0	0	1	0	1	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X17206	94.5	397	1	543	934	
79	00090	00078	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
80	00091	00079	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
81	00092	00080	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
82	00093	00081	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
83	00094	00082	9	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
84	00095	00083	62	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
85	00096	00084	62	6	5	4	2	0	0	0	1	2	6	5	1	3	1	5	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
86	00097	00085	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
87	00098	00086	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
88	00099	00087	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
89	00100	00088	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
90	00101	00089	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
91	00102	00090	44	2	4	0	3	0	1	1	1	6	2	1	2	8	0	1	1	4	0	0	0	0	0	0	0	0	0	0	X64707	93.3	387	1	346	942
92	00103	00091	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
93	00104	00092	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

Table 3

Table 4

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	IA	KA	MA	QA	SA	LA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
130	00143	00129	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
131	00144	00130	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	00145	00131	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	00146	00132	8	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	00147	00133	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
135	00148	00134	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
136	00149	00135	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
137	00150	00136	17	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	00151	00137	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
139	00152	00138	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	00153	00139	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	00154	00140	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	00155	00141	81	1	0	3	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	00156	00142	20	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	00157	00143	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	00158	00144	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	00159	00145	4	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	00160	00146	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	00161	00147	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	00162	00148	47	1	1	4	3	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	00163	00149	30	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
151	00164	00150	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	00165	00151	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	00166	00152	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	00167	00153	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
155	00168	00154	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
156	00169	00155	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	00170	00156	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	00171	00157	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	00172	00158	14	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	00173	00159	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	00174	00160	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	00175	00161	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	00176	00162	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	00177	00163	18	2	2	0	0	1	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	00178	00164	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 5



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	CA	CC	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
202	00217	00201	5	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203	00218	00202	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
204	00219	00203	13	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
205	00220	00204	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
206	00221	00205	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
207	00222	00206	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
208	00223	00207	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
209	00224	00208	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
210	00225	00209	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
211	00226	00210	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
212	00227	00211	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
213	00228	00212	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
214	00230	00213	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
215	00231	00214	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
216	00232	00215	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
217	00233	00216	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
218	00234	00217	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
219	00235	00218	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
220	00236	00219	11	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
221	00237	00220	11	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
222	00238	00221	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
223	00239	00222	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
224	00240	00223	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
225	00241	00224	12	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
226	00242	00225	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
227	00243	00226	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
228	00244	00227	65	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
229	00245	00228	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
230	00246	00229	26	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
231	00247	00230	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
232	00248	00231	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
233	00249	00232	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
234	00250	00233	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
235	00251	00234	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
236	00252	00235	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
237	00253	00236	16	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 7

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
238	00254	00237	38	1	0	0	2	0	0	1	2	1	0	1	0	2	0	1	3	0	0	0	0	0	1	3	20	0	M24096	98.1	214	1	1152	1365
239	00255	00238	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
240	00256	00239	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
241	00257	00240	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
242	00258	00241	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
243	00259	00242	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
244	00260	00243	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
245	00261	00244	17	2	1	0	1	0	1	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0						
246	00262	00245	50	2	7	2	0	1	1	2	0	3	6	0	1	3	0	0	3	0	1	2	0	0	4	0	6	2	M17885	99.6	211	1	888	1809
247	00263	00246	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
248	00264	00247	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
249	00265	00248	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
250	00266	00249	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
251	00267	00250	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
252	00268	00251	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
253	00269	00252	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
254	00270	00253	9	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
255	00271	00254	24	2	0	0	1	2	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
256	00272	00255	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
257	00273	00256	119	9	6	4	13	2	11	2	1	12	14	0	6	0	0	0	0	0	0	0	0	0	0	0	0							
258	00274	00257	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
259	00275	00258	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
260	00276	00259	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
261	00277	00260	36	3	0	0	0	0	8	14	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
262	00278	00261	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
263	00279	00262	10	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
264	00280	00263	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
265	00281	00264	8	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
266	00282	00265	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
267	00283	00266	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
268	00284	00267	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
269	00285	00268	89	6	14	1	8	0	3	4	1	4	4	3	5	3	5	0	2	5	1	1	4	1	3	2	0	8	1	0	0	0	0	0
270	00286	00269	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
271	00287	00270	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
272	00288	00271	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
273	00289	00272	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 8



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
274	00290	00273	85	5	9	3	8	4	2	1	1	1	7	4	1	4	5	0	2	6	5	3	6	1	0	2	0	5	0	X66699	99.5	184	1	163	349
275	00291	00274	8	1	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	
276	00292	00275	49	4	12	1	0	2	1	1	4	6	4	0	0	2	0	0	5	4	0	1	0	1	0	1	0	0	0	0	0	0	0	0	
277	00293	00276	74	6	13	1	6	2	4	3	3	2	5	0	1	0	4	0	0	2	2	0	0	0	1	5	0	11	3	0	0	0	0	0	
278	00294	00277	5	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	
279	00295	00278	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
280	00296	00279	8	1	4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	
281	00297	00280	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
282	00298	00281	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
283	00299	00282	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
284	00300	00283	24	2	1	0	2	0	1	0	0	1	1	2	0	3	1	4	2	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	
285	00301	00284	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
286	00302	00285	4	1	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
287	00303	00286	17	2	2	0	0	0	0	1	0	0	2	0	0	0	0	0	1	2	0	1	0	0	0	0	0	2	2	0	0	0	0	0	
288	00304	00287	48	2	1	2	2	1	0	1	1	3	2	2	3	1	0	4	2	6	0	3	0	1	4	3	3	1	0	0	0	0	0	0	
289	00305	00288	46	1	6	0	2	2	3	1	2	1	4	4	2	2	0	3	0	1	4	1	0	2	2	1	2	0	0	0	0	0	0	0	
290	00306	00289	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
291	00307	00290	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
292	00308	00291	10	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	3	1	0	2	0	0	0	0	0	0	0	0	
293	00309	00292	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
294	00310	00293	6	1	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
295	00311	00294	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
296	00312	00295	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
297	00313	00296	17	1	0	1	0	1	0	0	1	0	0	0	0	1	0	2	2	1	0	3	2	0	0	0	2	0	0	0	0	0	0	0	
298	00314	00297	45	1	3	1	3	0	1	1	5	1	1	0	0	7	2	0	3	2	0	3	0	0	4	3	2	0	2	0	0	0	0	0	
299	00315	00298	21	3	4	1	0	0	1	0	1	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
300	00316	00299	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
301	00317	00300	10	1	0	0	0	0	3	2	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
302	00320	00301	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
303	00322	00302	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
304	00323	00303	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
305	00325	00304	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
306	00327	00305	20	1	3	1	0	0	1	2	0	0	0	0	0	0	2	1	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	
307	00328	00306	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
308	00329	00307	5	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
309	00330	00308	8	1	0	2	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 9

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
310	00331	00309	6	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
311	00332	00310	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
312	00333	00311	16	1	0	0	3	0	0	0	0	1	4	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
313	00334	00312	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
314	00335	00313	86	1	16	4	3	1	1	0	3	7	3	1	6	6	1	3	2	1	1	1	4	2	5	0	10	3	M36072	100	165	1	727	891
315	00336	00314	47	1	2	2	2	0	1	0	0	5	6	0	1	2	0	3	4	3	1	1	0	1	8	0	3	0	Z12962	96.3	162	1	308	478
316	00337	00315	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	
317	00338	00316	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
318	00339	00317	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
319	00340	00318	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
320	00341	00319	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
321	00342	00320	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
322	00343	00321	12	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
323	00344	00322	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
324	00346	00323	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
325	00347	00324	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
326	00348	00325	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
327	00349	00326	29	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
328	00350	00327	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
329	00351	00328	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
330	00352	00329	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
331	00353	00330	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
332	00354	00331	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
333	00355	00332	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
334	00356	00333	43	1	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
335	00357	00334	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
336	00358	00335	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
337	00359	00336	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
338	00360	00337	19	2	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
339	00361	00338	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
340	00362	00339	19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
341	00363	00340	29	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
342	00364	00341	632	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
343	00365	00342	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
344	00366	00343	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
345	00367	00344	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 10

Table 11

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
382	00405	00381	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
383	00406	00382	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
384	00407	00383	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
385	00408	00384	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
386	00409	00385	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
387	00410	00386	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
388	00411	00387	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
389	00412	00388	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
390	00413	00389	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
391	00414	00390	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
392	00415	00391	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
393	00416	00392	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
394	00417	00393	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
395	00418	00394	116	5	22	1	13	1	5	1	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
396	00419	00395	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
397	00420	00396	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
398	00421	00397	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
399	00422	00398	16	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
400	00423	00399	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
401	00424	00400	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
402	00425	00401	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
403	00426	00402	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
404	00427	00403	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
405	00428	00404	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
406	00429	00405	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
407	00430	00406	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
408	00431	00407	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
409	00433	00408	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
410	00434	00409	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
411	00435	00410	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
412	00436	00411	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
413	00437	00412	34	5	4	2	2	0	0	0	2	1	0	2	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
414	00438	00413	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
415	00439	00414	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
416	00440	00415	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
417	00441	00416	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 12

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK		
418	00442	00417	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
419	00443	00418	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
420	00444	00419	71	6	10	1	4	2	4	1	1	0	3	1	0	5	0	0	1	4	8	5	5	0	3	5	0	2	0	98.9	90	1	410	510
421	00445	00420	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
422	00446	00421	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
423	00447	00422	38	2	6	1	1	0	3	2	0	6	2	0	0	1	0	0	3	1	1	0	1	1	0	3	0	0	96.5	86	1	841	926	
424	00448	00423	17	1	0	1	1	0	0	0	0	1	2	0	0	1	0	1	0	2	0	1	2	0	0	1	1	0						
425	00450	00424	30	3	2	2	0	0	0	0	0	0	0	0	0	2	1	0	2	0	3	1	10	0	2	0	0	0						
426	00451	00425	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
427	00453	00426	4	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
428	00454	00427	7	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
429	00455	00428	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
430	00456	00429	18	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
431	00457	00430	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
432	00458	00431	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
433	00459	00432	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
434	00460	00433	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
435	00461	00434	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
436	00462	00435	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
437	00463	00436	26	2	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
438	00464	00437	18	1	1	2	0	0	1	0	0	1	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
439	00465	00438	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
440	00466	00439	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
441	00467	00440	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
442	00468	00441	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
443	00469	00442	6	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
444	00470	00443	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
445	00471	00444	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
446	00473	00445	10	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
447	00474	00446	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
448	00475	00447	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
449	00477	00448	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
450	00478	00449	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
451	00479	00450	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
452	00480	00451	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
453	00481	00452	24	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 13

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
454	00482	00453	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0
455	00483	00454	5	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
456	00484	00455	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
457	00485	00456	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
458	00486	00457	6	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
459	00487	00458	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
460	00488	00459	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
461	00489	00460	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
462	00491	00461	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
463	00493	00462	4	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
464	00494	00463	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
465	00495	00464	12	1	2	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
466	00496	00465	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
467	00497	00466	11	1	1	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
468	00498	00467	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
469	00500	00468	54	6	4	1	1	0	2	2	3	3	2	3	1	1	0	3	8	1	2	1	1	1	1	0	4	1	0	1	438	488	
470	00503	00469	8	1	2	0	0	0	1	0	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
471	00504	00470	56	1	5	1	0	0	1	1	0	2	2	2	3	4	2	1	6	2	3	3	2	0	13	0	1	0	0	0	0	0	0
472	00505																																

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK			
490	00545	00489	36		3	0	2	0	0	2	1	2	3	0	1	3	1	1	0	2	1	1	0	1	3	0	7	1	M94314	93.4	439	1	75	556		
491	00546	00490	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
492	00547	00491	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
493	00548	00492	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M64716	94.4	478	2	24	497		
494	00549	00493	2		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
495	00551	00494	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
496	00552	00495	4		1	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
497	00553	00496	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
498	00554	00497	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
499	00555	00498	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
500	00556	00499	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D14662	97.5	481	1	395	1653		
501	00557	00500	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
502	00558	00501	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
503	00560	00502	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
504	00561	00503	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
505	00562	00504	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
506	00564	00505	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
507	00565	00506	70		4	2	5	0	1	1	1	1	1	4	5	1	1	0	4	6	2	1	1	2	0	0	25	0	2	M30684	96.4	415	1	519	929	
508	00567	00507	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L06432	95.9	98	162	332	549	
509	00568	00508	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
510	00569	00509	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
511	00571	00510	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
512	00572	00511	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
513	00573	00512	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
514	00574	00513	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
515	00575	00514	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J04564	93.5	370	4	736	1099	
516	00576	00515	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
517	00577	00516	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
518	00578	00517	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
519	00579	00518	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X52317	96.5	342	1	40	869	
520	00580	00519	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
521	00581	00520	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
522	00582	00521	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
523	00583	00522	34		2	5	3	0	0	0	1	3	1	3	0	2	1	4	0	0	0	0	0	0	0	0	0	0	0	0	X73460	95.8	378	1	900	1272
524	00584	00523	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
525	00585	00524	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

Table 15

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
526	00586	00525	6		1	0	0	1	1	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	X07674	95.5	396	1	2559	2970	
527	00589	00526	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
528	00590	00527	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
529	00591	00528	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M96954	97.2	351	1	1045	1401	
530	00592	00529	15		1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M84643	96.7	331	1	174	506	
531	00593	00530	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
532	00594	00531	17		3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M14199	99.7	341	1	136	475	
533	00595	00532	4		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M00282	98.5	344	1	1968	2509	
534	00596	00533	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
535	00597	00534	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
536	00598	00535	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
537	00599	00536	4		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
538	00600	00537	12		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
539	00601	00538	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
540	00602	00539	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
541	00603	00540	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
542	00604	00541	4		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
543	00606	00542	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
544	00607	00543	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
545	00608	00544	22		5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
546	00609	00545	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
547	00610	00546	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
548	00611	00547	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
549	00612	00548	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
550	00614	00549	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
551	00615	00550	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
552	00616	00551	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
553	00617	00552	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
554	00618	00553	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
555	00619	00554	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
556	00620	00555	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
557	00621	00556	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
558	00622	00557	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
559	00623	00558	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
560	00624	00559	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
561	00625	00560	4		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 16



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
562	00626	00561	4	2	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
563	00627	00562	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
564	00628	00563	4	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
565	00629	00564	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
566	00630	00565	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
567	00631	00566	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
568	00632	00567	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
569	00633	00568	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
570	00634	00569	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
571	00635	00570	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
572	00636	00571	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
573	00637	00572	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
574	00638	00573	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
575	00639	00574	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
576	00640	00575	10	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
577	00641	00576	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
578	00642	00577	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
579	00643	00578	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
580	00644	00579	24	5	0	2	0	1	1	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
581	00645	00580	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
582	00646	00581	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
583	00647	00582	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
584	00648	00583	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
585	00649	00584	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
586	00650	00585	52	14	2	6	0	2	0	1	1	1	2	1	6	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
587	00651	00586	9	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
588	00652	00587	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
589	00653	00588	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
590	00654	00589	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
591	00655	00590	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
592	00657	00591	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
593	00658	00592	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
594	00659	00593	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
595	00661	00594	9	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
596	00662	00595	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
597	00663	00596	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 17

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
598	00564	00597	3		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
599	00565	00598	2		1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
600	00566	00599	5		1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
601	00567	00600	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
602	00568	00601	8		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
603	00569	00602	2		1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
604	00570	00603	12		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
605	00571	00604	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
606	00572	00605	7		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
607	00573	00606	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
608	00574	00607	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
609	00575	00608	31		4	1	4	0	1	0	2	1	1	0	0	0	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
610	00576	00609	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
611	00577	00610	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
612	00578	00611	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
613	00579	00612	15		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
614	00580	00613	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
615	00581	00614	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
616	00582	00615	3		3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
617	00583	00616	20		1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
618	00584	00617	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
619	00585	00618	18		2	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
620	00586	00619	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
621	00587	00620	16		1	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
622	00588	00621	40		1	1	2	0	1	3	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
623	00590	00622	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
624	00591	00623	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
625	00592	00624	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
626	00593	00625	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
627	00594	00626	3		2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
628	00595	00627	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
629	00596	00628	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
630	00597	00629	7		2	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
631	00598	00630	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
632	00599	00631	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
633	00700	00632	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 18

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK
670	00739	00669	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
671	00740	00670	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
672	00671	00671	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
673	00742	00672	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
674	00743	00673	54	7	1	7	2	6	1	0	1	8	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
675	00745	00674	4	1	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
676	00746	00675	13	1	1	2	1	0	0	0	0	0	0	0	1	0	2	0	1	0	1	1	1	2	0	0	0	0	0	0	0	0	
677	00747	00676	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
678	00748	00677	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
679	00749	00678	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
680	00750	00679	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
681	00751	00680	5	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
682	00752	00681	4	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
683	00753	00682	6	2	0	0	0	0	0	0	0	0	0	0	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
684	00754	00683	5	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
685	00755	00684	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
686	00757	00685	5	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
687	00758	00686	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
688	00759	00687	25	4																													

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
706	00779	00705	3		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X5568	92.6	149	1	824	965		
707	00780	00706	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X70944	100	152	1	2916	3071		
708	00781	00707	1			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
709	00782	00708	8	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
710	00783	00709	5	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
711	00784	00710	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
712	00785	00711	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	145	1	329	491		
713	00786	00712	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
714	00787	00713	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
715	00788	00714	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
716	00789	00715	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
717	00790	00716	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M5502	96.5	141	1	1310	1447	
718	00791	00717	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X59417	96.6	149	1	824	979	
719	00792	00718	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
720	00793	00719	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
721	00794	00720	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
722	00795	00721	42	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
723	00796	00722	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
724	00797	00723	36	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L14754	98.5	133	1	3761	3892	
725	00798	00724	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X02984	100	137	1	362	498	
726	00799	00725	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
727	00800	00726	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X63423	94.3	141	1	545	691
728	00801	00727	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
729	00802	00728	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X04823	99.2	132	1	342	472
730	00803	00729	7	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
731	00804	00730	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
732	00805	00731	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
733	00806	00732	7	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
734	00807	00733	23	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X69392	98.5	134	1	357	773
735	00808	00734	8	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
736	00809	00735	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
737	00810	00736	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
738	00811	00737	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
739	00813	00738	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
740	00814	00739	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
741	00815	00740	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 21

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	BA	GA	IA	KA	MA	QA	SA	LA	VA	WA	YA	B	BC	BE	BF	BG	BH	BI	BK
742	00816	00741	14		1	5	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	100	125	1	1507	1631	
743	00817	00742	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
744	00818	00743	20		1	1	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0						
745	00819	00744	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
746	00820	00745	18		1	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0						
747	00821	00746	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
748	00822	00747	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
749	00823	00748	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
750	00824	00749	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
751	00825	00750	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
752	00826	00751	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
753	00827	00752	3		1	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
754	00828	00753	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
755	00829	00754	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
756	00830	00755	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
757	00831	00756	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
758	00832	00757	6		1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
759	00833	00758	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
760	00834	00759	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
761	00835	00760	5		1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
762	00836	00761	8		1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
763	00837	00762	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
764	00839	00763	7		1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
765	00840	00764	8		1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
766	00841	00765	10		5	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
767	00842	00766	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
768	00843	00767	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
769	00844	00768	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
770	00845	00769	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
771	00846	00770	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
772	00847	00771	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
773	00848	00772	12		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
774	00849	00773	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
775	00850	00774	12		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
776	00851	00775	14		5	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
777	00852	00776	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 22

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
778	00853	00777	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
779	00854	00778	8		1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
780	00855	00779	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
781	00856	00780	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
782	00857	00781	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
783	00858	00782	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
784	00859	00783	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
785	00860	00784	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
786	00861	00785	34		6	0	2	1	0	0	1	4	1	0	2	3	0	1	1	0	1	1	0	3	0	6	0	0	0	0	0	0	0	0	
787	00862	00786	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
788	00863	00787	5		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
789	00864	00788	5		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
790	00865	00789	56		9	2	1	0	0	0	2	8	2	1	4	1	0	3	5	4	0	0	0	9	2	0	1	0	0	0	0	0	0	0	0
791	00866	00790	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
792	00867	00791	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
793	00868	00792	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
794	00869	00793	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
795	00870	00794	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
796	00871	00795	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
797	00872	00796	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
798	00873	00797	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
799	00874	00798	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
800	00875	00799	21		2	3	1	1	0	0	0	0	0	0	0	3	0	1	6	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
801	00876	00800	9		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
802	00877	00801	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
803	00878	00802	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
804	00879	00803	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
805	00880	00804	5		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
806	00882	00805	20		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
807	00883	00806	5		1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
808	00884	00807	3		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
809	00885	00808	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
810	00886	00809	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
811	00887	00810	14		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
812	00889	00811	17		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
813	00890	00812	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 23

[illegible]



[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AC	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
886	0009	0085	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
887	0100	0086	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
888	0101	0087	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
889	0102	0088	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
890	0103	0089	5	0	0	1	0	0	0	1	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
891	0105	0090	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
892	0106	0091	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
893	0107	0092	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
894	0108	0093	6	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
895	0109	0094	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
896	0120	0095	8	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
897	0121	0096	9	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
898	0123	0097	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
899	0124	0098	6	0	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
900	0125	0099	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
901	0126	0090	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
902	0127	0091	4	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
903	0128	0092	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
904	0129	0093	13	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
905	0130	0094	9	0	0	2	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
906	0132	0095	14	0	0	2	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
907	0133	0096	3	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
908	0134	0097	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
909	0135	0098	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
910	0136	0099	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
911	0137	00910	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
912	0138	00911	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
913	0139	00912	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
914	0140	00913	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
915	0141	00914	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
916	0142	00915	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
917	0143	00916	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
918	0144	00917	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
919	0145	00918	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
920	0146	00919	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
921	0147	00920	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
922	01048	00921	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	M84694	96.9	382	1	708	1089
923	01049	00922	2		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
924	01051	00923	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
925	01052	00924	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
926	01053	00925	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M92423	90.3	380	24	371	4221
927	01054	00926	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
928	01055	00927	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
929	01057	00928	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
930	01061	00929	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M74782	98.3	347	1	1115	1460
931	01062	00930	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M06599	97.2	394	1	1011	1441
932	01063	00931	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
933	01064	00932	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
934	01065	00933	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
935	01066	00934	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
936	01067	00935	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
937	01068	00936	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
938	01069	00937	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
939	01070	00938	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
940	01071	00939	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
941	01072	00940	8		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
942	01073	00941	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
943	01074	00942	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M63071	97.3	377	1	4591	4972
944	01075	00943	10		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
945	01076	00944	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
946	01077	00945	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
947	01078	00946	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
948	01079	00947	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
949	01080	00948	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
950	01081	00949	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
951	01082	00950	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
952	01083	00951	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
953	01084	00952	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
954	01085	00953	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
955	01086	00954	8		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
956	01087	00955	18		0	6	0	0	0	0	0	0	0	0	0	0	0	0</														

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AN	AO	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK			
958	01089	00957	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	M16592	91.8	367	1	1410	1926		
959	01090	00958	2		0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
960	01091	00959	5		0	3	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
961	01092	00960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D12502	93	343	16	1	1391		
962	01093	00961	2		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
963	01094	00962	2		0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
964	01095	00963	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	96.9	193	1	1981	2371	
965	01096	00964	9		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
966	01097	00965	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
967	01098	00966	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	64	1	477	540	
968	01099	00967	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.9	354	3	1513	1894	
969	01100	00968	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
970	01101	00969	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
971	01102	00970	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
972	01103	00971	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
973	01104	00972	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
974	01105	00973	8		0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
975	01106	00974	16		0	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
976	01107	00975	11		0	2	0	0	0	0	0	3	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
977	01108	00976	5		0	1	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
978	01109	00977	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
979	01110	00978	2		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
980	01111	00979	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
981	01112	00980	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
982	01115	00981	2		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
983	01116	00982	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
984	01117	00983	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
985	01118	00984	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
986	01119	00985	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
987	01120	00986	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
988	01122	00987	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
989	01123	00988	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
990	01126	00989	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
991	01137	00990	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
992	01128	00991	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
993	01129	00992	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
994	01130	00993	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
995	01131	00994	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
996	01132	00995	3		0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
997	01133	00996	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
998	01134	00997	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
999	01135	00998	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1000	01136	00999	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1001	01137	01000	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1002	01138	01001	6		0	1	1	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
1003	01139	01002	3		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
1004	01140	01003	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1005	01141	01004	18		0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1006	01142	01005	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1007	01143	01006	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1008	01144	01007	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1009	01145	01008	7		0	4	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1010	01147	01009	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1011	01148	01010	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1012	01149	01011	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1013	01150	01012	6		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1014	01151	01013	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1015	01152	01014	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1016	01153	01015	3		0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1017	01154	01016	17		0	2	1	1	0	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1018	01155	01017	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1019	01156	01018	2		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1020	01157	01019	9		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1021	01158	01020	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1022	01159	01021	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1023	01160	01022	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1024	01161	01023	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1025	01162	01024	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1026	01163	01025	16		0	1	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1027	01164	01026	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1028	01165	01027	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1029	01167	01028	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 29

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1030	01168	01029	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
1031	01169	01030	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
1032	01170	01031	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1033	01171	01032	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1034	01172	01033	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1035	01173	01034	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1036	01174	01035	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1037	01175	01036	14		0	1	2	1	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X76717	98.9 275	1	21	415	
1038	01176	01037	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1039	01177	01038	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1040	01178	01039	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1041	01179	01040	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1042	01180	01041	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1043	01181	01042	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1044	01182	01043	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1045	01183	01044	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1046	01184	01045	7		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1047	01186	01046	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1048	01187	01047	8		0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1049	01188	01048	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M83246	97.9 285	1	1055	1349	
1050	01189	01049	13		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1051	01191	01050	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1052	01192	01051	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1053	01193	01052	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1054	01194	01053	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1055	01195	01054	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M94083	96 278	1	1374	1685	
1056	01196	01055	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1057	01197	01056	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1058	01198	01057	10		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Y00281	92.8 290	1	1934	2397	
1059	01199	01058	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1060	01200	01059	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1061	01201	01060	4		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1062	01202	01061	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1063	01203	01062	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M32011	94.6 276	1	1931	2206	
1064	01204	01063	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1065	01205	01064	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 30

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
1102	01244	01101	25		0	3	1	0	0	0	0	2	2	0	3	2	2	0	0	2	1	0	0	4	0	2	1	0	0	0	13585	93.5	262	1	254	518
1103	01245	01102	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1104	01246	01103	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1105	01247	01104	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1106	01248	01105	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1107	01249	01106	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1108	01250	01107	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1109	01251	01108	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1110	01252	01109	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1111	01253	01110	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1112	01254	01111	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1113	01255	01112	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1114	01257	01113	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1115	01258	01114	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1116	01259	01115	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1117	01260	01116	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1118	01261	01117	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1119	01262	01118	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1120	01263	01119	5		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1121	01264	01120	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1122	01265	01121	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1123	01266	01122	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1124	01267	01123	15		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1125	01268	01124	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1126	01269	01125	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1127	01270	01126	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1128	01272	01127	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1129	01273	01128	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1130	01274	01129	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1131	01276	01130	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1132	01277	01131	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1133	01278	01132	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1134	01279	01133	6		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1135	01280	01134	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1136	01281	01135	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1137	01282	01136	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 32



[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1174	01319	01173	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1175	01320	01174	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1176	01321	01175	19		0	3	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1177	01322	01176	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1178	01323	01177	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1179	01324	01178	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1180	01325	01179	17		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1181	01326	01180	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1182	01327	01181	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1183	01328	01182	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1184	01329	01183	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1185	01330	01184	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1186	01331	01185	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1187	01332	01186	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1188	01333	01187	1		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1189	01334	01188	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1190	01335	01189	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1191	01336	01190	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1192	01337	01191	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1193	01338	01192	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1194	01339	01193	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1195	01340	01194	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1196	01341	01195	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1197	01342	01196	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1198	01343	01197	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1199	01344	01198	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1200	01345	01199	4		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1201	01346	01200	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1202	01347	01201	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1203	01348	01202	13		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1204	01349	01203	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1205	01350	01204	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1206	01351	01205	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1207	01352	01206	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1208	01353	01207	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1209	01354	01208	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 34

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1210	01355	01209	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1211	01356	01210	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1212	01357	01211	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1213	01358	01212	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1214	01359	01213	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1215	01360	01214	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1216	01361	01215	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1217	01362	01216	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1218	01363	01217	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1219	01364	01218	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1220	01365	01219	4	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1221	01366	01220	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1222	01367	01221	21	0	3	1	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1223	01368	01222	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1224	01369	01223	5	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1225	01370	01224	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1226	01371	01225	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1227	01372	01226	7	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1228	01373	01227	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1229	01374	01228	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1230	01375	01229	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1231	01377	01230	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1232	01378	01231	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1233	01379	01232	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1234	01380	01233	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1235	01381	01234	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1236	01382	01235	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1237	01383	01236	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1238	01384	01237	16	0	1	1	0	0	0	0	2	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1239	01385	01238	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1240	01386	01239	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1241	01387	01240	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1242	01388	01241	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1243	01389	01242	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1244	01390	01243	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1245	01391	01244	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 35

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1246	01392	01245	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	505
1247	01393	01246	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67
1248	01394	01247	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1249	01395	01248	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1250	01396	01249	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1724
1251	01397	01250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1875
1252	01398	01251	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1253	01400	01252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1254	01401	01253	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1255	01402	01254	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1256	01403	01255	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1257	01404	01256	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1258	01405	01257	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1551
1259	01406	01258	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2577
1260	01407	01259	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1261	01408	01260	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1262	01409	01261	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1263	01410	01262	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1264	01411	01263	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1265	01412	01264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1266	01413	01265	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1267	01414	01266	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1268	01415	01267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1269	01416	01268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1270	01417	01269	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1271	01418	01270	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1272	01419	01271	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1273	01420	01272	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1274	01421	01273	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1275	01422	01274	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1276	01423	01275	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1277	01424	01276	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1278	01426	01277	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1279	01427	01278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1280	01428	01279	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1281	01429	01280	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 36

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1282	01430	01281	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3	144	1	1470	1612
1283	01431	01282	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1284	01432	01283	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1285	01433	01284	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1286	01434	01285	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1287	01435	01286	7		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1288	01436	01287	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1289	01437	01288	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1290	01438	01289	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1291	01439	01290	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1292	01440	01291	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1293	01441	01292	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1294	01442	01293	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1295	01443	01294	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1296	01444	01295	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1297	01445	01296	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1298	01446	01297	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1299	01447	01298	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1300	01448	01299	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1301	01449	01300	10		0	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1302	01450	01301	4		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1303	01451	01302	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1304	01452	01303	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1305	01453	01304	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1306	01454	01305	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1307	01455	01306	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1308	01456	01307	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1309	01457	01308	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1310	01458	01309	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1311	01459	01310	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1312	01460	01311	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1313	01461	01312	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1314	01462	01313	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1315	01463	01314	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1316	01464	01315	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1317	01465	01316	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 37

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1318	01467	01317	4	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
1319	01468	01318	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1320	01469	01319	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1321	01470	01320	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1322	01471	01321	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1323	01472	01322	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1324	01473	01323	9	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1325	01474	01324	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1326	01475	01325	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1327	01476	01326	19	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1328	01477	01327	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1329	01478	01328	5	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1330	01479	01329	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1331	01481	01330	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1332	01482	01331	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1333	01483	01332	9	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1334	01484	01333	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1335	01485	01334	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1336	01486	01335	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1337	01487	01336	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1338	01488	01337	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1339	01489	01338	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1340	01490	01339	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1341	01491	01340	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1342	01492	01341	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1343	01493	01342	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1344	01494	01343	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1345	01495	01344	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1346	01496	01345	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1347	01497	01346	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1348	01498	01347	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1349	01499	01348	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1350	01500	01349	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1351	01501	01350	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1352	01502	01351	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1353	01503	01352	9	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 38

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK	
1354	01595	01353	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1355	01596	01354	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X55187	98.3	406	1	1923	2327	
1356	01597	01355	5	0	0	1	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	M25064	99.1	112	1	1617	1760	
1357	01598	01356	13	0	0	3	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1358	01599	01357	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1359	01510	01358	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1360	01511	01359	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1361	01512	01360	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1362	01513	01361	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1363	01514	01362	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1364	01515	01363	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1365	01516	01364	7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M73554	93.6	110	1	3448	4221	
1366	01517	01365	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1367	01518	01366	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1368	01519	01367	3	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1369	01520	01368	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1370	01521	01369	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1371	01522	01370	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1372	01523	01371	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1373	01524	01372	7	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1374	01525	01373	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1375	01526	01374	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1376	01527	01375	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1377	01528	01376	16	0	0	2	3	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1378	01529	01377	7	0	0	2	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1379	01530	01378	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1380	01531	01379	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1381	01532	01380	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1382	01533	01381	19	0	0	1	2	0	0	0	0	1	0	2	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1383	01534	01382	8	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1384	01535	01383	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1385	01537	01384	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1386	01538	01385	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1387	01539	01386	12	0	0	1	3	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1388	01540	01387	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1389	01541	01388	6	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1390	01542	01389	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1391	01543	01390	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1392	01544	01391	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1393	01545	01392	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1394	01546	01393	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1395	01547	01394	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1396	01548	01395	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1397	01549	01396	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1398	01550	01397	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1399	01551	01398	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1400	01552	01399	10	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1401	01553	01400	5	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1402	01554	01401	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1403	01555	01402	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1404	01556	01403	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1405	01557	01404	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1406	01558	01405	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1407	01560	01406	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1408	01561	01407	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1409	01562	01408	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1410	01563	01409	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1411	01564	01410	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1412	01565	01411	6	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1413	01566	01412	9	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1414	01567	01413	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1415	01568	01414	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1416	01569	01415	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1417	01570	01416	7	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1418	01571	01417	10	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1419	01572	01418	4	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1420	01573	01419	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1421	01574	01420	11	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1422	01575	01421	6	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1423	01576	01422	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1424	01577	01423	5	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1425	01578	01424	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 40



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
1426	01579	01425	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
1427	01580	01426	4		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
1428	01581	01427	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2634		
1429	01582	01428	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1430	01583	01429	5		0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3193		
1431	01584	01430	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1432	01585	01431	8		0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3683		
1433	01586	01432	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1434	01587	01433	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1435	01588	01434	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1436	01589	01435	10		0	1	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1437	01590	01436	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1438	01591	01437	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1439	01592	01438	4		0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1440	01593	01439	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1441	01594	01440	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1442	01595	01441	7		0	1	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100062		
1443	01596	01442	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1444	01597	01443	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1445	01598	01444	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1446	01599	01445	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1447	01600	01446	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1448	01601	01447	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1449	01602	01448	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1450	01603	01449	5		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1451	01604	01450	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1452	01605	01451	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1453	01606	01452	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1454	01607	01453	4		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1455	01608	01454	23		0	2	0	0	0	0	0	0	1	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	560099	
1456	01609	01455	16		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10052		
1457	01610	01456	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	560099	
1458	01611	01457	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10052	
1459	01612	01458	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1460	01614	01459	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1461	01615	01460	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 41

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1498	01703	01497	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1499	01704	01498	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1500	01705	01499	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1501	01706	01500	12		0	0	4	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1502	01707	01501	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1503	01708	01502	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1504	01709	01503	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1505	01710	01504	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1506	01711	01505	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1507	01713	01506	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1508	01714	01507	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1509	01715	01508	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1510	01718	01509	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1511	01719	01510	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1512	01720	01511	43		0	0	1	0	0	0	4	2	4	3	1	1	0	0	0	0	0	0	0	0	0	0	0						
1513	01721	01512	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1514	01722	01513	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1515	01724	01514	9		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1516	01726	01515	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1517	01727	01516	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1518	01728	01517	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1519	01729	01518	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1520	01730	01519	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1521	01731	01520	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1522	01732	01521	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1523	01733	01522	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1524	01734	01523	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1525	01735	01524	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1526	01736	01525	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1527	01737	01526	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1528	01738	01527	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1529	01739	01528	8		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1530	01740	01529	8		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1531	01741	01530	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1532	01742	01531	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1533	01745	01532	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 43

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
1534	01746	01533	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1535	01747	01534	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1536	01748	01535	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1537	01749	01536	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.7	358	1	850	2177	
1538	01750	01537	2		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2	358	1	278	637	
1539	01751	01538	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1540	01752	01539	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
1541	01753	01540	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1542	01754	01541	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1543	01755	01542	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1544	01756	01543	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1545	01758	01544	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1546	01759	01545	7		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1547	01760	01546	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1548	01761	01547	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1549	01763	01548	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1550	01764	01549	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1551	01765	01550	7		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1552	01766	01551	63		0	0	6	15	2	4	2	0	4	0	5	1	1	0	6	1	10	3	0	0	1	0	0	94.7	337	1	1615	1958
1553	01767	01552	3		0	0	1	0	0	0	0	0																				

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1570	01784	01569	2		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1571	01785	01570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1572	01786	01571	8		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1573	01787	01572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1574	01788	01573	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1575	01789	01574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1576	01790	01575	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1577	01791	01576	34		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1578	01792	01577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1579	01793	01578	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1580	01794	01579	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1581	01795	01580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1582	01796	01581	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1583	01797	01582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1584	01798	01583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1585	01799	01584	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1586	01800	01585	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1587	01801	01586	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1588	01802	01587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1589	01803	01588	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1590	01804	01589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1591	01805	01590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1592	01806	01591	26		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1593	01807	01592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1594	01808	01593	47		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1595	01809	01594	19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1596	01810	01595	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1597	01811	01596	39		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1598	01812	01597	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1599	01813	01598	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

Table 45

[illegible]

Table 46

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AV	AW	BA	BC	BE	BF	BG	BH	BI	BK	
1612	01856	01641	5		0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	M33146	100 186	6	1612	1797	
1613	01857	01642	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	
1614	01858	01643	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1615	01859	01644	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1616	01860	01645	4		0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1617	01861	01646	18		0	0	1	0	0	0	1	1	1	0	1	2	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1618	01862	01647	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1619	01863	01648	18		0	0	1	0	0	0	0	1	1	2	2	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1620	01864	01649	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1621	01865	01650	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1622	01866	01651	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1623	01867	01652	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1624	01868	01653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1625	01869	01654	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1626	01870	01655	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1627	01871	01656	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1628	01872	01657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1629	01873	01658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1630	01874	01659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1631	01875	01660	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1632	01876	01661	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1633	01877	01662	8		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1634	01878	01663	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1635	01880	01664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1636	01881	01665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1637	01882	01666	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1638	01883	01667	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1639	01884	01668	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1640	01885	01669	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1641	01886	01670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1642	01887	01671	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1643	01888	01672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1644	01889	01673	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1645	01890	01674	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1646	01891	01675	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1647	01892	01676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 47

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	A	A	C	A	I	A	K	A	M	A	C	A	S	A	L	A	W	A	B	C	B	E	B	F	B	G	B	H	B	I	B	K			
1678	01893	01677	1																																														
1679	01895	01678	7																																														
1680	01896	01679	2																																														
1681	01897	01680	1																																														
1682	01898	01681	1																																														
1683	01899	01682	14																																														
1684	01900	01683	1																																														
1685	01901	01684	1																																														
1686	01902	01685	2																																														
1687	01903	01686	2																																														
1688	01904	01687	3																																														
1689	01905	01688	3																																														
1690	01906	01689	3																																														
1691	01907	01690	1																																														
1692	01908	01691	21																																														
1693	01909	01692	4																																														
1694	01910	01693	1																																														
1695	01911	01694	10																																														
1696	01912	01695	5																																														
1697	01913	01696	2																																														
1698	01914	01697	3																																														
1699	01915	01698	1																																														
1700	01916	01699	3																																														
1701	01917	01700	1																																														
1702	01918	01701	2																																														
1703	01919	01702	111																																														
1704	01920	01703	1																																														
1705	01921	01704	1																																														
1706	01922	01705	3																																														
1707	01923	01706	2																																														
1708	01924	01707	3																																														
1709	01925	01708	1																																														
1710	01926	01709	24																																														
1711	01927	01710	3																																														
1712	01928	01711	10																																														
1713	01929	01712	19																																														

Table 48



[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK				
1786	02007	01785	15		0	0	1	0	0	0	1	0	2	0	0	0	0	2	0	1	4	0	0	1	0	0	0	0	69023	100	56	1	1064	1119	
1787	02010	01786	7	0	0	0	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0		
1788	02011	01787	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0		
1789	02012	01788	16	0	0	0	2	2	0	0	2	0	1	0	1	0	0	0	0	1	0	1	1	3	0	0	1	0	0	0	0	0	0	0	
1790	02013	01789	12	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	
1791	02025	01790	8	0	0	1	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1792	02039	01791	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1793	02040	01792	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1794	02041	01793	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1795	02042	01794	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1796	02043	01795	8	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1797	02044	01796	5	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1798	02045	01797	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1799	02046	01798	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1800	02047	01799	13	0	0	0	2	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1801	02048	01800	5	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1802	02049	01801	20	0	0	0	1	0	0	1	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1803	02050	01802	5	0</																															

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
1822	02070	01821	2		0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
1823	02071	01822	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1824	02072	01823	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1825	02073	01824	16		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1826	02074	01825	7		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1827	02075	01826	7		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1828	02076	01827	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1829	02077	01828	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1830	02078	01829	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1831	02079	01830	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1832	02080	01831	11		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1833	02081	01832	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1834	02082	01833	7		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1835	02084	01834	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1836	02085	01835	83		0	0	0	0	16	26	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1837	02086	01836	4		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1838	02087	01837	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1839	02088	01838	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1840	02089	01839	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1841	02090	01840	1		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1842	02091	01841	9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1843	02092	01842	11		0	0	0	0	2	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1844	02093	01843	11		0	0	0	0	2	3	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1845	02094	01844	6		0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1846	02095	01845	2		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1847	02096	01846	2		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1848	02097	01847	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1849	02098	01848	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1850	02099	01849	3		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1851	02100	01850	5		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1852	02101	01851	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1853	02102	01852	5		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1854	02103	01853	5		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1855	02104	01854	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1856	02105	01855	109		0	0	0	0	6	4	3	10	0	36	22	0	0	0	0	0	0	0	0	0	0	0	0	0					
1857	02106	01856	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 52

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	ABC	DE	BF	BG	BH	BI	BK
1858	02107	01857	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1859	02108	01858	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1860	02110	01859	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1861	02111	01860	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1862	02112	01861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1863	02113	01862	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1864	02115	01863	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1865	02116	01864	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1866	02117	01865	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1867	02118	01866	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1868	02119	01867	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1869	02120	01868	19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1870	02121	01869	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1871	02122	01870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1872	02123	01871	28		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1873	02124	01872	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1874	02126	01873	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1875	02127	01874	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1876	02128	01875	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1877	02129	01876	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1878	02130	01877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1879	02131	01878	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1880	02132	01879	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1881	02133	01880	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1882	02134	01881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1883	02135	01882	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1884	02136	01883	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1885	02137	01884	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1886	02138	01885	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1887	02139	01886	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1888	02140	01887	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1889	02141	01888	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1890	02142	01889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1891	02143	01890	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1892	02144	01891	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1893	02145	01892	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 53

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1930	02182	01929	3						1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1931	02183	01930	3						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1932	02184	01931	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1933	02185	01932	3						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1934	02186	01933	68						1	1	2	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	96	99	1	1551	1676	
1935	02187	01934	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1936	02188	01935	2						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1937	02189	01936	11						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1938	02191	01937	6						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1939	02192	01938	2						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98	8	83	1	842	923
1940	02193	01939	3						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1941	02194	01940	2						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97	8	91	1	1606	2593
1942	02195	01941	8						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97	3	73	11	2040	2113
1943	02196	01942	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1944	02197	01943	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1945	02198	01944	2						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1946	02199	01945	5						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	76	1	2451	2544	
1947	02200	01946	6						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	60	1	8480	8878	
1948	02202	01947	32						15	12	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1949	02203	01948	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1950	02204	01949	3						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1951	02205	01950	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1952	02206	01951	4						2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1953	02207	01952	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1954	02208	01953	2						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1955	02209	01954	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1956	02210	01955	3						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1957	02211	01956	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1958	02212	01957	2						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98	2	57	1	143	282
1959	02213	01958	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1960	02214	01959	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1961	02215	01960	4						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1962	02216	01961	2						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1963	02217	01962	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93	1	101	1	5116	5215
1964	02218	01963	1						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1965	02219	01964	6						1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97	3	447	1	964	1418

Table 55

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
1966	02240	01965	5		0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1967	02241	01966	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1968	02242	01967	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1969	02243	01968	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1970	02244	01969	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1971	02245	01970	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1972	02246	01971	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1973	02247	01972	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1974	02248	01973	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1975	02249	01974	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1976	02250	01975	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1977	02252	01976	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1978	02254	01977	3	3	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1979	02255	01978	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1980	02256	01979	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1981	02257	01980	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1982	02258	01981	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1983	02259	01982	10	10	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1984	02260	01983	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1985	02261	01984	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1986	02262	01985	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1987	02263	01986	4	4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1988	02264	01987	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1989	02266	01988	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1990	02268	01989	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1991	02269	01990	4	4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1992	02270	01991	3	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1993	02271	01992	12	12	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1994	02272	01993	9	9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1995	02274	01994	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1996	02275	01995	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1997	02276	01996	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1998	02277	01997	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1999	02278	01998	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2000	02279	01999	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2001	02280	02000	3	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 56



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
2002	02281	02001	1																													
2003	02282	02002	1																													
2004	02283	02003	1																													
2005	02285	02004	10																													
2006	02287	02005	1																													
2007	02288	02006	1																													
2008	02289	02007	1																													
2009	02290	02008	16																													
2010	02291	02009	1																													
2011	02292	02010	1																													
2012	02293	02011	1																													
2013	02294	02012	1																													
2014	02295	02013	1																													
2015	02296	02014	2																													
2016	02297	02015	2																													
2017	02298	02016	1																													
2018	02299	02017	4																													
2019	02300	02018	3																													
2020	02301	02019	1																													
2021	02302	02020	5																													
2022	02303	02021	1																													
2023	02304	02022	1																													
2024	02305	02023	2																													
2025	02306	02024	1																													
2026	02307	02025	1																													
2027	02308	02026	3																													
2028	02309	02027	18																													
2029	02310	02028	3																													
2030	02311	02029	6																													
2031	02312	02030	5																													
2032	02313	02031	6																													
2033	02314	02032	2																													
2034	02315	02033	1																													
2035	02316	02034	12																													
2036	02317	02035	5																													
2037	02318	02036	2																													

Table 57

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AY	B	BC	BE	BF	BG	BI	BK
2074	02358	02073	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2075	02359	02074	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2076	02360	02075	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2077	02361	02076	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2078	02362	02077	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2079	02363	02078	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2080	02364	02079	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2081	02365	02080	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2082	02366	02081	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2083	02367	02082	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2084	02368	02083	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2085	02369	02084	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2086	02370	02085	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2087	02371	02086	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2088	02372	02087	6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2089	02373	02088	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2090	02374	02089	38		0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2091	02375	02090	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2092	02376	02091	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2093	02377	02092	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2094	02378	02093	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2095	02379	02094	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2096	02380	02095	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2097	02382	02096	13		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2098	02399	02097	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2099	02400	02098	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2100	02401	02099	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2101	02402	02100	6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2102	02403	02101	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2103	02404	02102	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2104	02406	02103	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2105	02408	02104	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2106	02409	02105	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2107	02411	02106	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2108	02412	02107	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2109	02413	02108	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 59

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK	
2110	02414	02109	2		0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		97.9	340	1	1994	2798
2111	02415	02110	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2112	02416	02111	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2113	02417	02112	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2114	02418	02113	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2115	02419	02114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2116	02420	02115	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2117	02421	02116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2118	02422	02117	7		0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0						
2119	02423	02118	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2120	02424	02119	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2121	02425	02120	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2122	02426	02121	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2123	02427	02122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2124	02428	02123	4		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2125	02429	02124	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2126	02430	02125	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2127	02431	02126	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2128	02432	02127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2129	02433	02128	2		0	0	0	0	0																							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	B	BC	BE	BF	BG	BI	BK
2146	02452	02145	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2147	02453	02146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2148	02454	02147	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2149	02455	02148	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2150	02456	02149	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2151	02457	02150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2152	02458	02151	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2153	02459	02152	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2154	02461	02153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2155	02462	02154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2156	02463	02155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2157	02464	02156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2158	02465	02157	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2159	02466	02158	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2160	02467	02159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2161	02468	02160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2162	02469	02161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2163	02471	02162	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2164	02472	02163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2165	02473	02164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2166	02474	02165	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2167	02475	02166	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2168	02476	02167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2169	02477	02168	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2170	02478	02169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2171	02479	02170	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2172	02480	02171	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2173	02481	02172	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2174	02482	02173	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2175	02483	02174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2176	02484	02175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2177	02486	02176	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2178	02487	02177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2179	02488	02178	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2180	02489	02179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2181	02490	02180	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 61

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AF	AG	AH	AI	AK	AM	AN	AO	AS	AT	AV	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
2182	02491	02181	4		0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2183	02493	02182	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2184	02494	02183	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2185	02495	02184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2186	02496	02185	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2187	02497	02186	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2188	02498	02187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2189	02499	02188	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2190	02500	02189	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2191	02501	02190	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2192	02502	02191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2193	02503	02192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2194	02504	02193	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2195	02505	02194	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2196	02506	02195	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2197	02507	02196	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2198	02508	02197	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2199	02509	02198	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2200	02510	02199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2201	02511	02200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2202	02512	02201	13		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2203	02513	02202	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2204	02514	02203	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2205	02515	02204	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2206	02516	02205	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2207	02517	02206	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2208	02518	02207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2209	02519	02208	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2210	02520	02209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2211	02521	02210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2212	02522	02211	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2213	02523	02212	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2214	02524	02213	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2215	02525	02214	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2216	02526	02215	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2217	02527	02216	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 62

[illegible]

Table 63

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	FA	GA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BG	BI	BJ	BK
2254	02573	02553	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2255	02574	02254	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2256	02575	02255	3		0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2257	02576	02256	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2258	02577	02257	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2259	02578	02258	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2260	02580	02259	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2261	02581	02260	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2262	02582	02261	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2263	02583	02262	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2264	02585	02263	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2265	02586	02264	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2266	02588	02265	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2267	02589	02266	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2268	02590	02267	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2269	02591	02268	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2270	02592	02269	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2271	02593	02270	2		0	0	0	0	0																									



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2290	02645	02289	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2291	02646	02290	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2292	02648	02291	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2293	02650	02292	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2294	02651	02293	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2295	02652	02294	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2296	02653	02295	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2297	02654	02296	2		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2298	02656	02297	20		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2299	02657	02298	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2300	02658	02299	6		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2301	02659	02300	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2302	02660	02301	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2303	02661	02302	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2304	02662	02303	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2305	02663	02304	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2306	02664	02305	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2307	02665	02306	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2308	02666	02307	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2309	02667	02308	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2310	02668	02309	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2311	02669	02310	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2312	02670	02311	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2313	02672	02312	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2314	02673	02313	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2315	02675	02314	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2316	02676	02315	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2317	02677	02316	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2318	02678	02317	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2319	02679	02318	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2320	02680	02319	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2321	02681	02320	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2322	02682	02321	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2323	02684	02322	13		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2324	02685	02323	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2325	02686	02324	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 65

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2326	02687	02325	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2327	02688	02326	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2328	02689	02327	4		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2329	02690	02328	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2330	02691	02329	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2331	02692	02330	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2332	02693	02331	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2333	02694	02332	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2334	02695	02333	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2335	02696	02334	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2336	02697	02335	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2337	02698	02336	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2338	02699	02337	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2339	02700	02338	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2340	02701	02339	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2341	02702	02340	5		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2342	02703	02341	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2343	02704	02342	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2344	02705	02343	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2345	02706	02344	13		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2346	02707	02345	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2347	02708	02346	8		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2348	02709	02347	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2349	02710	02348	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2350	02711	02349	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2351	02712	02350	8		0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2352	02713	02351	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2353	02714	02352	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2354	02715	02353	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2355	02716	02354	18		0	0	0	0	0	0	2	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2356	02717	02355	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2357	02718	02356	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2358	02719	02357	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2359	02721	02358	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2360	02722	02359	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2361	02723	02360	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 66

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CC	GG	II	LL	MM	NN	PP	RR	SS	TT	VV	XX	YY	ZZ	BE	BF	BG	BI	BI	BK
2470	02839	02469	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2471	02840	02470	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2472	02843	02471	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2473	02844	02472	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2474	02845	02473	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2475	02846	02474	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2476	02847	02475	11		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2477	02848	02476	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2478	02849	02477	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2479	02850	02478	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2480	02851	02479	9		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2481	02852	02480	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2482	02853	02481	8		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2483	02854	02482	4		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2484	02855	02483	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2485	02856	02484	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2486	02857	02485	3		0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2487	02858	02486	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2488	02859	02487	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2489	02860	02488	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2490	02861	02489	10		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2491	02862	02490	7		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2492	02863	02491	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2493	02864	02492	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2494	02865	02493	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2495	02866	02494	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2496	02867	02495	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2497	02868	02496	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2498	02869	02497	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2499	02870	02498	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2500	02872	02499	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2501	02873	02500	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2502	02874	02501	6		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2503	02875	02502	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2504	02876	02503	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2505	02877	02504	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 70

[illegible]







[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
2650	03086	02649	5		0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3	298	1	394	691
2651	03087	02650	8		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	545630					
2652	03088	02651	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2653	03089	02652	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2654	03090	02653	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2655	03091	02654	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2656	03092	02655	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2657	03094	02656	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2658	03095	02657	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.1	279	1	159	1187
2659	03096	02658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2660	03097	02659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2661	03098	02660	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2662	03099	02661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2663	03100	02662	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2664	03101	02663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2665	03102	02664	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2666	03103	02665	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2667	03104	02666	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2668	03105	02667	15		0	0	0	0	0	0	0	2	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2669	03106	02668	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2670	03108	02669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2671	03109	02670	13		0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2672	03110	02671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2673	03111	02672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2674	03112	02673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2675	03115	02674	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2676	03116	02675	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2677	03117	02676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2678	03118	02677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2679	03119	02678	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2680	03120	02679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2681	03121	02680	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2682	03122	02681	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2683	03123	02682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0													

Table 75

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2722	03169	02721	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
2723	03170	02722	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2724	03171	02723	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
2725	03172	02724	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.5	174		1 2728	2900	
2726	03173	02725	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2727	03175	02726	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2728	03176	02727	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2729	03177	02728	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2730	03178	02729	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2731	03179	02730	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2732	03180	02731	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2733	03181	02732	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2734	03182	02733	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2735	03183	02734	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2736	03185	02735	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2737	03186	02736	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2738	03187	02737	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2739	03188	02738	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2740	03189	02739	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2741	03190	02740	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2742	03192	02741	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2743	03193	02742	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2744	03194	02743	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2745	03195	02744	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2746	03196	02745	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2747	03197	02746	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2748	03198	02747	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2749	03200	02748	52		0	0	0	0	0	0	0	4	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2750	03201	02749	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2751	03202	02750	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2752	03204	02751	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2753	03205	02752	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2754	03206	02753	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2755	03207	02754	9		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2756	03208	02755	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2757	03212	02756	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 77

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BAB	BC	BE	BF	BGBH	BI	BK	
2758	03213	02757	3		0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
2759	03214	02758	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2760	03215	02759	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2761	03216	02760	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.3	406	1	3055	3634
2762	03217	02761	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2763	03218	02762	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2764	03219	02763	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2765	03220	02764	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2766	03221	02765	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2767	03222	02766	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2768	03223	02767	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2769	03224	02768	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	124	1	2325	2463
2770	03225	02769	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2771	03227	02770	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2772	03229	02771	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2773	03230	02772	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2774	03231	02773	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2775	03233	02774	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2776	03234	02775	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2777	03235	02776	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2778	03236	02777	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2779	03237	02778	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2780	03239	02779	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2781	03240	02780	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2782	03241	02781	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2783	03242	02782	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2784	03243	02783	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2785	03244	02784	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2786	03245	02785	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2787	03247	02786	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2788	03248	02787	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2789	03249	02788	6		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2790	03251	02789	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2791	03252	02790	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2792	03253	02791	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2793	03255	02792	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 78

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2830	03326	02829	1																														
2831	03331	02830	24																														
2832	03332	02831	6																														
2833	03356	02832	2																														
2834	03374	02833	1																														
2835	03375	02834	1																														
2836	03376	02835	2																														
2837	03377	02836	4																														
2838	03378	02837	1																														
2839	03379	02838	3																														
2840	03380	02839	1																														
2841	03381	02840	3																														
2842	03382	02841	3																														
2843	03383	02842	1																														
2844	03384	02843	3																														
2845	03385	02844	1																														
2846	03386	02845	2																														
2847	03387	02846	1																														
2848	03388	02847	3																														
2849	03389	02848	1																														
2850	03390	02849	1																														
2851	03391	02850	2																														
2852	03392	02851	1																														
2853	03393	02852	1																														
2854	03394	02853	7																														
2855	03395	02854	3																														
2856	03396	02855	2																														
2857	03397	02856	1																														
2858	03398	02857	1																														
2859	03399	02858	2																														
2860	03400	02859	1																														
2861	03401	02860	1																														
2862	03402	02861	5																														
2863	03403	02862	4																														
2864	03404	02863	2																														
2865	03405	02864	1																														

Table 80



[illegible]

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2902	03443	02901	14	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2903	03444	02902	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2904	03445	02903	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2905	03446	02904	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2906	03447	02905	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2907	03448	02906	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2908	03449	02907	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2909	03450	02908	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2910	03451	02909	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2911	03452	02910	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2912	03453	02911	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2913	03454	02912	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2914	03455	02913	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2915	03456	02914	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2916	03457	02915	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2917	03458	02916	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2918	03459	02917	7	0	0	0	0	0	0	0	0	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2919	03460	02918	8	0	0	0	0	0	0	0	0	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2920	03461	02919	5	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2921	03462	02920	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2922	03463	02921	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2923	03464	02922	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2924	03465	02923	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2925	03466	02924	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2926	03467	02925	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2927	03468	02926	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2928	03469	02927	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2929	03470	02928	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2930	03471	02929	6	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2931	03472	02930	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2932	03473	02931	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2933	03474	02932	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2934	03476	02933	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2935	03477	02934	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2936	03478	02935	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2937	03479	02936	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 82

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	CA	CC	AS	AL	AW	AY	BA	BC	BE	BF	BG	BI	CK
2974	03516	02973	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
2975	03517	02974	10	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
2976	03518	02975	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	M5929	100	96	1	1335
2977	03519	02976	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
2978	03520	02977	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2979	03521	02978	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	560099	97.6	166	1	2428
2980	03522	02979	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2981	03523	02980	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2982	03524	02981	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2983	03525	02982	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2984	03526	02983	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2985	03527	02984	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2986	03528	02985	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2987	03529	02986	6	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2988	03530	02987	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2989	03531	02988	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2990	03532	02989	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2991	03533	02990	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2992	03534	02991	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0																

[illegible]

Table 85

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
3046	03588	03045	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3047	03589	03046	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3048	03590	03047	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3049	03591	03048	9		0	0	0	0	0	0	0	0	2	0	0	0	1	0	2	0	0	2	0	0	0	0	1	0.06328	97.8	179	1	1061	1404	
3050	03592	03049	2		0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	97.1	238	1	2559	3075	
3051	03593	03050	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3052	03594	03051	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3053	03595	03052	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3054	03596	03053	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3055	03597	03054	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3056	03598	03055	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3057	03599	03056	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3058	03600	03057	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3059	03602	03058	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3060	03603	03059	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3061	03604	03060	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3062	03605	03061	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0						
3063	03606	03062	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3064	03607	03063	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0																

Table 87

[illegible]



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
3154	03723	03153	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3155	03724	03154	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3156	03725	03155	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3157	03726	03156	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
3158	03727	03157	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3159	03728	03158	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3160	03729	03159	3		0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3161	03730	03160	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3162	03731	03161	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0					
3163	03732	03162	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3164	03733	03163	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3165	03734	03164	7		0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	3					
3166	03736	03165	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3167	03737	03166	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3168	03738	03167	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3169	03739	03168	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3170	03740	03169	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3171	03741	03170	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3172	03742	03171	3		0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3173	03743	03172	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3174	03744	03173	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
3175	03745	03174	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3176	03746	03175	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3177	03747	03176	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3178	03748	03177	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3179	03749	03178	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3180	03750	03179	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3181	03751	03180	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3182	03752	03181	8		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3183	03753	03182	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3184	03754	03183	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3185	03755	03184	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3186	03756	03185	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3187	03757	03186	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3188	03758	03187	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3189	03759	03188	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK
3190	03760	03189	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3191	03761	03190	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3192	03762	03191	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3193	03763	03192	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3194	03764	03193	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3195	03765	03194	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3196	03766	03195	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3197	03767	03196	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3198	03768	03197	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3199	03769	03198	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3200	03770	03199	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3201	03771	03200	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3202	03772	03201	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3203	03773	03202	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3204	03774	03203	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3205	03775	03204	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3206	03776	03205	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3207	03777	03206	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3208	03778	03207	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3209	03779	03208	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3210	03780	03209	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3211	03781	03210	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3212	03782	03211	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3213	03783	03212	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3214	03784	03213	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3215	03785	03214	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3216	03786	03215	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3217	03787	03216	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3218	03788	03217	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3219	03789	03218	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3220	03790	03219	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3221	03791	03220	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3222	03792	03221	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3223	03793	03222	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3224	03794	03223	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3225	03795	03224	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 90

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BI	BK
3226	03796	03225	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3227	03797	03226	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3228	03798	03227	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3229	03799	03228	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3230	03800	03229	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3231	03801	03230	3											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3232	03802	03231	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3233	03803	03232	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3234	03804	03233	7											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3235	03805	03234	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3236	03806	03235	3											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3237	03807	03236	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3238	03808	03237	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3239	03809	03238	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3240	03810	03239	1											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3241	03811	03240	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3242	03812	03241	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3243	03813	03242	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3244	03814	03243	6											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3245	03815	03244	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3246	03816	03245	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3247	03817	03246	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3248	03818	03247	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3249	03819	03248	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3250	03820	03249	3											2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3251	03821	03250	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3252	03822	03251	5											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3253	03823	03252	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3254	03824	03253	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3255	03825	03254	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3256	03826	03255	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3257	03827	03256	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3258	03828	03257	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3259	03829	03258	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3260	03830	03259	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3261	03831	03260	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 91

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3262	03832	03261	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3263	03833	03262	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3264	03835	03263	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3265	03836	03264	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3266	03837	03265	13		0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0						
3267	03838	03266	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3268	03839	03267	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3269	03840	03268	1		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0						
3270	03841	03269	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3271	03842	03270	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3272	03843	03271	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3273	03844	03272	50		0	0	0	0	0	0	0	0	0	25	0	0	0	0	0	0	0	0	0	0	0	0	0						
3274	03845	03273	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3275	03846	03274	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3276	03847	03275	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3277	03848	03276	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3278	03849	03277	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3279	03850	03278	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3280	03851	03279	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3281	03852	03280	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3282	03853	03281	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3283	03854	03282	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3284	03855	03283	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3285	03856	03284	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3286	03857	03285	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3287	03859	03286	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3288	03860	03287	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3289	03861	03288	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3290	03862	03289	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3291	03863	03290	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3292	03864	03291	6		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
3293	03865	03292	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3294	03866	03293	3		0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0						
3295	03867	03294	20		0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0						
3296	03868	03295	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3297	03869	03296	7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 92

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AN	AO	AP	AS	AT	AW	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK
3298	03870	03297	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3299	03871	03298	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3300	03872	03299	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3301	03873	03300	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3302	03874	03301	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3303	03875	03302	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3304	03876	03303	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3305	03877	03304	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3306	03878	03305	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3307	03879	03306	7		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3308	03880	03307	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3309	03881	03308	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3310	03882	03309	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3311	03883	03310	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3312	03884	03311	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3313	03885	03312	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3314	03886	03313	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3315	03887	03314	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3316	03888	03315	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3317	03889	03316	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3318	03890	03317	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3319	03891	03318	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3320	03892	03319	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3321	03893	03320	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3322	03894	03321	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3323	03895	03322	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3324	03896	03323	7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3325	03897	03324	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3326	03898	03325	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3327	03899	03326	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3328	03900	03327	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3329	03901	03328	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3330	03902	03329	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3331	03903	03330	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3332	03904	03331	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3333	03905	03332	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

[illegible]

Table 94

[illegible]

[illegible]



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	RE	BF	BG	BH	BI	BK
3442	04051	03441	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	M10051	100	154	1	2017	4723	
3443	04052	03442			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3444	04053	03443	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
3445	04054	03444	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3446	04055	03445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3447	04056	03446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3448	04057	03447	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3449	04058	03448	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3450	04059	03449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3451	04060	03450	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3452	04061	03451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3453	04062	03452	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3454	04063	03453	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3455	04064	03454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3456	04065	03455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3457	04066	03456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3458	04067	03457	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3459	04068	03458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3460	04069	03459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3461	04070	03460	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3462	04071	03461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3463	04072	03462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3464	04073	03463	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3465	04074	03464	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3466	04075	03465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3467	04076	03466	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3468	04077	03467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3469	04078	03468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3470	04079	03469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3471	04080	03470	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3472	04081	03471	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3473	04082	03472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3474	04083	03473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3475	04084	03474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3476	04085	03475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3477	04087	03476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 97

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3478	04088	03477	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	95.6	271	1	2937	3554
3479	04089	03478	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	96.7	270	1	3174	4108
3480	04090	03479	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	99.6	264	1	594	870
3481	04091	03480	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	99.2	260	1	221	480
3482	04092	03481	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	98.8	250	1	836	1104
3483	04093	03482	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3484	04094	03483	13		0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0					
3485	04095	03484	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3486	04096	03485	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3487	04097	03486	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3488	04098	03487	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3489	04099	03488	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	94.7	246	1	2377	2798
3490	04100	03489	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3491	04101	03490	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3492	04102	03491	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3493	04103	03492	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3494	04104	03493	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3495	04105	03494	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3496	04106	03495	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3497	04107	03496	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3498	04108	03497	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3499	04109	03498	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3500	04110	03499	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3501	04111	03500	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3502	04112	03501	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3503	04113	03502	4		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0					
3504	04114	03503	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3505	04115	03504	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3506	04116	03505	12		0	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0					
3507	04117	03506	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3508	04118	03507	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3509	04119	03508	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3510	04120	03509	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0					
3511	04121	03510	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3512	04122	03511	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3513	04123	03512	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					

Table 98

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGRH	BI	BK
3514	04125	03513	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3515	04126	03514	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3516	04127	03515	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3517	04128	03516	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3518	04129	03517	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3519	04130	03518	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3520	04131	03519	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3521	04132	03520	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3522	04133	03521	7		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3523	04134	03522	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3524	04135	03523	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3525	04136	03524	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3526	04137	03525	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3527	04139	03526	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3528	04140	03527	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3529	04141	03528	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3530	04142	03529	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3531	04143	03530	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3532	04144	03531	11		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3533	04145	03532	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3534	04146	03533	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3535	04147	03534	6		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3536	04148	03535	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3537	04149	03536	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3538	04150	03537	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3539	04151	03538	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3540	04152	03539	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3541	04153	03540	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3542	04154	03541	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3543	04155	03542	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3544	04156	03543	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3545	04157	03544	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3546	04158	03545	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3547	04159	03546	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3548	04160	03547	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3549	04161	03548	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					

Table 99

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	FA	GA	IA	KA	MA	QA	SA	TA	VA	WA	XA	YA	Z	BE	BF	BG	BH	BI	BK
3586	04201	03585	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3587	04202	03586	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3588	04203	03587	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3589	04204	03588	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3590	04205	03589	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0							
3591	04206	03590	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3592	04207	03591	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3593	04210	03592	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3594	04211	03593	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3595	04213	03594	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3596	04214	03595	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3597	04215	03596	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3598	04216	03597	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3599	04218	03598	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3600	04219	03599	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3601	04220	03600	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3602	04247	03601	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3603	04248	03602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3604	04249	03603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3605	04250	03604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3606	04252	03605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3607	04253	03606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3608	04256	03607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3609	04257	03608	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3610	04258	03609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3611	04259	03610	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3612	04261	03611	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3613	04264	03612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3614	04265	03613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3615	04266	03614	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3616	04267	03615	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3617	04268	03616	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3618	04269	03617	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3619	04270	03618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3620	04271	03619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3621	04272	03620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 101

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3622	04273	03621	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3623	04274	03622	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3624	04275	03623	2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3625	04276	03624	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3626	04278	03625	4	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3627	04279	03626	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3628	04280	03627	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3629	04281	03628	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3630	04282	03629	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3631	04284	03630	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3632	04285	03631	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3633	04286	03632	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3634	04287	03633	2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3635	04288	03634	3	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3636	04289	03635	2	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3637	04290	03636	8	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3638	04291	03637	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3639	04292	03638	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3640	04293	03639	2	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3641	04294	03640	6	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3642	04295	03641	2	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3643	04296	03642	2	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3644	04297	03643	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3645	04298	03644	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3646	04299	03645	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3647	04300	03646	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3648	04302	03647	2	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3649	04303	03648	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3650	04304	03649	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3651	04305	03650	3	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3652	04306	03651	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3653	04307	03652	2	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3654	04308	03653	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3655	04309	03654	2	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3656	04310	03655	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3657	04311	03656	3	3	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 102

[illegible]

[illegible]



[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BI	BI	BK
3766	04425	03765	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3767	04426	03766	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3768	04427	03767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3769	04428	03768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3770	04429	03769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3771	04430	03770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3772	04431	03771	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3773	04432	03772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3774	04433	03773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3775	04434	03774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3776	04435	03775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3777	04436	03776	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3778	04437	03777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3779	04439	03778	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3780	04440	03779	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3781	04441	03780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3782	04442	03781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3783	04443	03782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3784	04445	03783	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3785	04446	03784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3786	04447	03785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3787	04448	03786	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3788	04449	03787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3789	04450	03788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3790	04452	03789	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3791	04453	03790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3792	04454	03791	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3793	04455	03792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3794	04456	03793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3795	04457	03794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3796	04460	03795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3797	04462	03796	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3798	04463	03797	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3799	04464	03798	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3800	04465	03799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3801	04466	03800	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 106

[illegible]

[illegible]

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[illegible]

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[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3982	04706	03981	3		0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0	94.3	230	1	1045	1292
3983	04707	03982	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3984	04708	03983	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3985	04709	03984	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3986	04710	03985	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3987	04711	03986	7		0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0					
3988	04712	03987	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3989	04713	03988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3990	04714	03989	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3991	04715	03990	5		0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0					
3992	04716	03991	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3993	04717	03992	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3994	04718	03993	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3995	04719	03994	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3996	04720	03995	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3997	04721	03996	4		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0					
3998	04722	03997	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3999	04723	03998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4000	04724	03999	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
4001	04725	04000																														



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4018	04745	04017	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4019	04746	04018	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4020	04747	04019	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4021	04748	04020	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4022	04750	04021	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4023	04751	04022	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4024	04752	04023	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4025	04753	04024	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4026	04754	04025	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4027	04755	04026	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4028	04756	04027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4029	04757	04028	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4030	04758	04029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4031	04759	04030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4032	04760	04031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4033	04761	04032	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4034	04762	04033	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4035	04763	04034	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4036	04764	04035	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4037	04765	04036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4038	04766	04037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4039	04767	04038	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4040	04768	04039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4041	04769	04040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4042	04770	04041	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4043	04771	04042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4044	04772	04043	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4045	04773	04044	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4046	04774	04045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4047	04775	04046	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4048	04776	04047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4049	04777	04048	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4050	04778	04049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4051	04779	04050	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4052	04780	04051	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4053	04781	04052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 113



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[illegible]

Table 117

[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	A	A	C	A	I	A	K	A	M	A	C	A	S	A	L	A	W	A	B	A	B	C	B	E	D	F	B	G	B	H	I	B	K			
4270	05076	04269	2																																															
4271	05077	04270	1																																															
4272	05079	04271	1																																															
4273	05080	04272	1																																															
4274	05081	04273	2																																															
4275	05082	04274	2																																															
4276	05083	04275	1																																															
4277	05085	04276	4																																															
4278	05086	04277	2																																															
4279	05087	04278	1																																															
4280	05088	04279	1																																															
4281	05089	04280	1																																															
4282	05090	04281	2																																															
4283	05092	04282	1																																															
4284	05094	04283	1																																															
4285	05095	04284	1																																															
4286	05096	04285	1																																															
4287	05099	04286	2																																															
4288	05100	04287	2																																															
4289	05102	04288	1																																															
4290	05103	04289	5																																															
4291	05104	04290	1																																															
4292	05105	04291	3																																															
4293	05106	04292	3																																															
4294	05107	04293	2																																															
4295	05108	04294	12																																															
4296	05109	04295	1																																															
4297	05110	04296	1																																															
4298	05111	04297	16																																															
4299	05112	04298	1																																															
4300	05113	04299	1																																															
4301	05114	04300	1																																															
4302	05115	04301	2																																															
4303	05116	04302	1																																															
4304	05117	04303	1																																															
4305	05118	04304	2																																															

Table 120



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	GA	IA	KA	MA	CA	AS	AL	AV	AW	BA	BC	BE	BF	BG	BH	BI	BK
4306	05119	04305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4307	05120	04306	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4308	05121	04307	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4309	05122	04308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4310	05123	04309	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4311	05124	04310	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4312	05127	04311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4313	05128	04312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4314	05129	04313	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4315	05130	04314	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4316	05132	04315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4317	05133	04316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4318	05134	04317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4319	05135	04318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4320	05136	04319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4321	05137	04320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4322	05138	04321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4323	05139	04322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4324	05140	04323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4325	05141	04324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4326	05142	04325	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4327	05143	04326	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4328	05144	04327	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4329	05145	04328	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4330	05147	04329	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4331	05148	04330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4332	05149	04331	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4333	05150	04332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4334	05151	04333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4335	05152	04334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4336	05153	04335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4337	05155	04336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4338	05157	04337	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4339	05158	04338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4340	05159	04339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4341	05160	04340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 121

Table 122

[illegible]



[illegible]

Table 125



































	A	B	C	F	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BI	BK
5026	06000	05025	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5027	06001	05026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5028	06004	05027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5029	06005	05028	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5030	06008	05029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5031	06010	05030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5032	06011	05031	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5033	06013	05032	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5034	06014	05033	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5035	06015	05034	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5036	06016	05035	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5037	06017	05036	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5038	06018	05037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5039	06020	05038	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5040	06021	05039	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5041	06022	05040	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5042	06023	05041	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5043	06024	05042	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5044	06025	05043	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5045	06026	05044	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5046	06027	05045	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5047	06028	05046	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5048	06030	05047	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5049	06031	05048	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5050	06032	05049	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5051	06034	05050	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5052	06035	05051	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5053	06036	05052	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5054	06038	05053	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5055	06039	05054	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5056	06040	05055	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5057	06041	05056	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5058	06042	05057	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5059	06043	05058	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5060	06044	05059	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5061	06045	05060	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 141





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5134	06129	05133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5135	06130	05134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5136	06131	05135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5137	06133	05136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5138	06136	05137	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5139	06137	05138	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0							
5140	06138	05139	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0							
5141	06139	05140	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0							
5142	06141	05141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5143	06142	05142	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5144	06144	05143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5145	06145	05144	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5146	06146	05145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5147	06148	05146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5148	06150	05147	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5149	06151	05148	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5150	06152	05149	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5151	06153	05150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5152	06154	05151	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5153	06155	05152	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5154	06156	05153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5155	06157	05154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5156	06158	05155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5157	06159	05156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5158	06160	05157	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5159	06161	05158	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5160	06163	05159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5161	06164	05160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0							
5162	06165	05161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5163	06166	05162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5164	06167	05163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5165	06168	05164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5166	06169	05165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5167	06170	05166	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5168	06171	05167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5169	06172	05168	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							

Table 144









	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	IA	JA	KA	MA	QA	SA	TA	WA	YA	BA	CA	DA	BF	BG	BI	BK	
5278	06299	05277	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.7	229	1	2508	2736
5279	06300	05278	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.9	176	1	1256	1766
5280	06301	05279	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5281	06302	05280	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5282	06303	05281	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5283	06304	05282	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5284	06305	05283	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5285	06306	05284	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5286	06307	05285	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5287	06308	05286	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5288	06309	05287	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5289	06310	05288	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5290	06311	05289	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5291	06313	05290	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5292	06314	05291	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5293	06315	05292	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5294	06316	05293	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5295	06317	05294	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5296	063																																	







	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
S422	06434	05421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	L10910	95.1	205	1	2334	2595	
S423	06455	05422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S424	06456	05423	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S425	06457	05424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S426	06458	05425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S427	06459	05426	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S428	06460	05427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	MS9465	100	183	1	4244	4426	
S429	06461	05428	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S430	06462	05429	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S431	06463	05430	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S432	06464	05431	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S433	06465	05432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S434	06466	05433	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S435	06468	05434	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S436	06469	05435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S437	06470	05436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S438	06471	05437	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S439	06472	05438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
S440	06473	05439	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0						
S441	06474	05440	1		0																												



Table 153

[illegible]

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Table 155

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5566	06615	05565	1																														
5567	06616	05566	1																														
5568	06617	05567	1																														
5569	06618	05568	2																									98.7	76	1	4882	4957	
5570	06619	05569	1																														
5571	06620	05570	1																														
5572	06621	05571	1																														
5573	06623	05572	1																														
5574	06624	05573	2																														
5575	06625	05574	1																														
5576	06626	05575	1																														
5577	06627	05576	1																														
5578	06628	05577	1																														
5579	06630	05578	1																														
5580	06631	05579	1																														
5581	06632	05580	1																														
5582	06633	05581	1																														
5583	06634	05582	1																														
5584	06635	05583	2																														
5585	06636	05584	2																														
5586	06637	05585	1																														
5587	06638	05586	1																														
5588	06639	05587	2																														
5589	06640	05588	1																														
5590	06641	05589	1																														
5591	06642	05590	1																														
5592	06643	05591	1																														
5593	06645	05592	1																														
5594	06646	05593	1																														
5595	06647	05594	1																														
5596	06649	05595	1																														
5597	06650	05596	2																														
5598	06651	05597	1																														
5599	06652	05598	1																														
5600	06653	05599	1																														
5601	06654	05600	1																														

Table 156

[illegible]









Table 161

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BAB	BC	BE	BF	BG	BH	BI	BK
5782	06859	05781	2																														
5783	06863	05782	1																														
5784	06864	05783	1																														
5785	06865	05784	1																														
5786	06866	05785	1																														
5787	06869	05786	4																														
5788	06870	05787	1																														
5789	06871	05788	1																														
5790	06872	05789	1																														
5791	06873	05790	1																														
5792	06874	05791	1																														
5793	06875	05792	1																														
5794	06876	05793	1																														
5795	06878	05794	1																														
5796	06879	05795	1																														
5797	06880	05796	1																														
5798	06882	05797	2																														
5799	06883	05798	1																														
5800	06884	05799	1																														
5801	06885	05800	2																														
5802	06886	05801	1																														
5803	06888	05802	1																														
5804	06889	05803	1																														
5805	06890	05804	1																														
5806	06891	05805	1																														
5807	06893	05806	1																														
5808	06894	05807	1																														
5809	06895	05808	1																														
5810	06896	05809	1																														
5811	06897	05810	1																														
5812	06898	05811	1																														
5813	06899	05812	1																														
5814	06900	05813	1																														
5815	06901	05814	1																														
5816	06902	05815	1																														
5817	06903	05816	1																														

[illegible]



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5890	06995	05889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5891	06996	05890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5892	06997	05891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5893	06998	05892	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5894	06999	05893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5895	07000	05894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5896	07001	05895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5897	07002	05896	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5898	07003	05897	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5899	07004	05898	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5900	07005	05899	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5901	07006	05900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5902	07007	05901	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5903	07008	05902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5904	07009	05903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5905	07011	05904	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5906	07012	05905	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5907	07013	05906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5908	07014	05907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5909	07015	05908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5910	07016	05909	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5911	07017	05910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5912	07018	05911	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5913	07020	05912	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5914	07021	05913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5915	07022	05914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5916	07023	05915	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5917	07025	05916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5918	07026	05917	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5919	07027	05918	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5920	07028	05919	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5921	07029	05920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5922	07030	05921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5923	07031	05922	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5924	07032	05923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	J	A	C	A	I	A	K	A	C	A	S	A	L	A	W	A	B	C	B	F	B	G	I	H	B	I	B	K	
6034	07158	06033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6035	07160	06034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6036	07161	06035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6037	07162	06036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6038	07163	06037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6039	07164	06038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6040	07165	06039	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6041	07166	06040	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6042	07167	06041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6043	07169	06042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6044	07170	06043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6045	07171	06044	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6046	07173	06045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6047	07174	06046	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6048	07175	06047	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
6049	07178	06048	1		0</																																						



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	A	C	A	E	A	C	A	M	A	C	A	C	A	S	A	L	A	W	A	Y	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL	BM	BN	BO	BP	BQ	BR	BS	BT	BU	BV	BW	BX	BY	BZ	CA	CB	CC	CD	CE	CF	CG	CH	CI	CJ	CK	CL	CM	CN	CO	CP	CQ	CR	CS	CT	CU	CV	CW	CX	CY	CZ	DA	DB	DC	DD	DE	DF	DG	DH	DI	DJ	DK	DL	DM	DN	DO	DP	DQ	DR	DS	DT	DU	DV	DW	DX	DY	DZ	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	IJ	JK	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LL	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MM	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NN	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI	OJ	OK	OL	OM	ON	OO	OP	OQ	OR	OS	OT	OU	OV	OW	OX	OY	OZ	PA	PB	PC	PD	PE	PF	PG	PH	PI	PJ	PK	PL	PM	PN	PO	PP	PQ	PR	PS	PT	PU	PV	PW	PX	PY	PZ	QA	QB	QC	QD	QE	QF	QG	QH	QI	QJ	QK	QL	QM	QN	QO	QP	QQ	QR	QS	QT	QU	QV	QW	QX	QY	QZ	RA	RB	RC	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RQ	RR	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SU	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TQ	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	VW	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ	WK	WL	WM	WN	WO	WP	WQ	WR	WS	WT	WU	WV	WW	WX	WY	WZ	XA	XB	XC	XD	XE	XF	XG	XH	XI	XJ	XK	XL	XM	XN	XO	XP	XQ	XR	XS	XT	XU	XV	XW	XX	XY	XZ	YA	YB	YC	YD	YE	YF	YG	YH	YI	YJ	YK	YL	YM	YN	YO	YP	YQ	YR	YS	YT	YU	YV	YW	YX	YY
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[illegible]

[illegible]









[illegible]

[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
50	6430	07595	06429	2																											
	6431	07596	06430	1																											
	6432	07597	06431	1																											
	6433	07598	06432	1																											
	6434	07599	06433	2																											
	6435	07600	06434	1																											
	6436	07601	06435	1																											
	6437	07602	06436	1																											
	6438	07603	06437	1																											
	6439	07604	06438	2																											
	6440	07605	06439	1																											
	6441	07606	06440	1																											
	6442	07607	06441	1																											
	6443	07608	06442	1																											
	6444	07609	06443	1																											
	6445	07610	06444	1																											
	6446	07611	06445	1																											
	6447	07612	06446	1																											
	6448	07613	06447	2																											
	6449	07614	06448	3																											
	6450	07615	06449	1																											
	6451	07616	06450	1																											
	6452	07617	06451	1																											
	6453	07619	06452	1																											
	6454	07620	06453	2																											
	6455	07621	06454	1																											
	6456	07622	06455	1																											
	6457	07623	06456	1																											
	6458	07624	06457	1																											
	6459	07625	06458	1																											
	6460	07626	06459	1																											
	6461	07627	06460	1																											
	6462	07628	06461	1																											
	6463	07629	06462	1																											
	6464	07630	06463	1																											
	6465	07631	06464	1																											

Table 180



[illegible]

Table 182

[illegible]

[illegible]



[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6646	07835	06645	1																														
6647	07836	06646	2																														
6648	07837	06647	1																														
6649	07838	06648	1																														
6650	07839	06649	2																														
6651	07840	06650	1																														
6652	07841	06651	3																														
6653	07844	06652	1																														
6654	07845	06653	1																														
6655	07848	06654	7																														
6656	07849	06655	1																														
6657	07850	06656	1																														
6658	07852	06657	1																														
6659	07853	06658	1																														
6660	07854	06659	2																														
6661	07855	06660	1																														
6662	07856	06661	1																														
6663	07857	06662	1																														
6664	07858	06663	1																														
6665	07859	06664	1																														
6666	07860	06665	1																														
6667	07861	06666	2																														
6668	07862	06667	1																														
6669	07863	06668	1																														
6670	07864	06669	1																														
6671	07865	06670	1																														
6672	07866	06671	2																														
6673	07868	06672	1																														
6674	07869	06673	1																														
6675	07870	06674	1																														
6676	07871	06675	1																														
6677	07872	06676	1																														
6678	07875	06677	1																														
6679	07876	06678	1																														
6680	07878	06679	1																														
6681	07879	06680	2																														

Table 187

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	DE	BF	BG	BH	BI	BK
6754	07971	06753	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6755	07973	06754	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6756	07974	06755	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6757	07975	06756	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6758	07976	06757	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6759	07977	06758	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6760	07981	06759	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6761	07986	06760	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6762	07987	06761	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6763	07988	06762	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6764	07989	06763	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6765	07990	06764	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6766	07991	06765	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6767	07992	06766	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6768	07994	06767	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6769	07995	06768	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6770	07997	06769	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6771	07998	06770	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6772	07999	06771	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
67																																	

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	EG	IA	KA	MA	NA	OA	QA	SA	TA	UA	VA	WA	XA	YA	ZA	BE	BF	BG	BH	BI	BK
6790	6817	3																													92.7	300	1	236	852		
6791	6818	1																																			
6792	6819	1																																			
6793	6820	1																																			
6794	6821	1																																			
6795	6822	1																																			
6796	6823	1																																			
6797	6824	1																																			
6798	6825	27																																			
6799	6826	1																																			
6800	6827	2																																			
6801	6828	1																																			
6802	6829	1																																			
6803	6830	2																																			
6804	6831	1																																			
6805	6832	1																																			
6806	6833	1																																			
6807	6834	1																																			
6808	6835	1																																			
6809	6836	1																																			
6810	6837	1																																			
6811	6838	1																																			
6812	6839	2																																			
6813	6840	1																																			

Table 191

Table 192



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6898	08128	06897	1																														
6899	08129	06898	1																														
6900	08130	06899	1																														
6901	08131	06900	1																														
6902	08132	06901	1																														
6903	08133	06902	1																														
6904	08134	06903	1																														
6905	08135	06904	2																														
6906	08136	06905	1																														
6907	08137	06906	1																														
6908	08138	06907	1																														
6909	08139	06908	1																														
6910	08140	06909	1																														
6911	08141	06910	1																														
6912	08142	06911	1																														
6913	08143	06912	1																														
6914	08144	06913	1																														
6915	08145	06914	1																														
6916	08146	06915	2																														
6917	08147	06916	1																														
6918	08148	06917	1																														
6919	08149	06918	1																														
6920	08150	06919	1																														
6921	08151	06920	1																														
6922	08153	06921	1																														
6923	08154	06922	2																														
6924	08155	06923	1																														
6925	08156	06924	1																														
6926	08157	06925	2																														
6927	08158	06926	1																														
6928	08159	06927	1																														
6929	08160	06928	1																														
6930	08161	06929	1																														
6931	08162	06930	2																														
6932	08163	06931	1																														
6933	08164	06932	1																														

Table 193

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK		
6934	08165	06933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	94.2	103	7	2589	2691
6935	08166	06934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6936	08167	06935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6937	08168	06936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6938	08169	06937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6939	08170	06938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6940	08172	06939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6941	08173	06940	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6942	08174	06941	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6943	08175	06942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6944	08176	06943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6945	08177	06944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6946	08178	06945	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6947	08179	06946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6948	08180	06947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6949	08181	06948	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0						
6950	08182	06949	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6951	08184	06950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6952	08185	06951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6953	08186	06952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6954	08188	06953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6955	08189	06954	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6956	08190	06955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6957	08191	06956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6958	08192	06957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6959	08193	06958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6960	08194	06959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6961	08195	06960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6962	08196	06961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6963	08197	06962	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6964	08198	06963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6965	08199	06964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6966	08200	06965	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6967	08201	06966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6968	08202	06967	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6969	08203	06968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						

Table 194

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AI	AK	AM	AO	AS	AW	AW	AY	B	BC	BE	BF	DG	BI	BI	BK
6970	08204	06969	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6971	08205	06970	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6972	08206	06971	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6973	08207	06972	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6974	08208	06973	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6975	08209	06974	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6976	08210	06975	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6977	08211	06976	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6978	08212	06977	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6979	08213	06978	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6980	08214	06979	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6981	08215	06980	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6982	08216	06981	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6983	08217	06982	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6984	08218	06983	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6985	08219	06984	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6986	08220	06985	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6987	08221	06986	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6988	08222	06987	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AT	BA	BB	BC	BE	BF	BG	BI	BK
7006	08241	07005	1																												
7007	08242	07006	1																												
7008	08243	07007	1																												
7009	08244	07008	1																												
7010	08245	07009	1																												
7011	08246	07010	1																												
7012	08247	07011	1																												
7013	08248	07012	1																												
7014	08249	07013	1																												
7015	08250	07014	2																												
7016	08251	07015	1																												
7017	08252	07016	1																												
7018	08253	07017	1																												
7019	08254	07018	1																												
7020	08255	07019	1																												
7021	08256	07020	1																												
7022	08257	07021	1																												
7023	08258	07022	1																												
7024	08259	07023	1																												
7025	08260	07024	1																												
7026	08261	07025	1																												
7027	08262	07026	1																												
7028	08263	07027	1																												
7029	08264	07028	1																												
7030	08265	07029	1																												
7031	08266	07030	1																												
7032	08267	07031	1																												
7033	08268	07032	1																												
7034	08269	07033	1																												
7035	08270	07034	1																												
7036	08271	07035	1																												
7037	08272	07036	1																												
7038	08273	07037	1																												
7039	08274	07038	1																												
7040	08275	07039	1																												
7041	08276	07040	1																												

Table 196



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AO	AS	AW	AY	BAB	BC	BE	BF	BG	BI	BK	
7078	08313	07077	1																													
7079	08314	07078	1																													
7080	08315	07079	1																													
7081	08316	07080	1																													
7082	08317	07081	1																													
7083	08318	07082	1																													
7084	08319	07083	2																													
7085	08320	07084	2																													
7086	08321	07085	1																													
7087	08322	07086	1																													
7088	08323	07087	1																													
7089	08324	07088	1																													
7090	08325	07089	4																													
7091	08326	07090	1																													
7092	08327	07091	1																													
7093	08328	07092	1																													
7094	08329	07093	1																													
7095	08330	07094	1																													
7096	08331	07095	1																													
7097	08332	07096	1																													
7098	08333	07097	1																													
7099	08334	07098	1																													
7100	08335	07099	1																													
7101	08336	07100	3																								XI7042	97.3	296	1	344	1182
7102	08337	07101	2																								H81637	93.9	295	1	1293	1652
7103	08338	07102	2																													
7104	08339	07103	9																													
7105	08340	07104	2																													
7106	08341	07105	1																													
7107	08342	07106	1																													
7108	08343	07107	1																													
7109	08344	07108	1																													
7110	08345	07109	1																													
7111	08346	07110	1																													
7112	08347	07111	8																													
7113	08348	07112	1																													

[illegible]

Table 199

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[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	FA	GA	IA	KA	MA	QA	SA	LA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
7258	08496	07357	1																															
7259	08497	07258	1																															
7260	08498	07259	1																															
7261	08499	07260	2																															
7262	08500	07261	1																															
7263	08501	07262	1																															
7264	08502	07263	1																															
7265	08503	07264	1																															
7266	08504	07265	1																															
7267	08505	07266	1																															
7268	08506	07267	1																															
7269	08507	07268	1																															
7270	08508	07269	1																															
7271	08509	07270	1																															
7272	08510	07271	1																															
7273	08511	07272	1																															
7274	08512	07273	2																															
7275	08513	07274	4																															
7276	08514	07275	1																															
7277	08515	07276	1																															
7278	08516	07277	1																															
7279	08517	07278	1																															
7280	08518	07279	1																															
7281	08519	07280	1																															
7282	08520	07281	1																															
7283	08521	07282	1																															
7284	08522	07283	1																															
7285	08523	07284	1																															
7286	08524	07285	1																															
7287	08525	07286	1																															
7288	08526	07287	1																															
7289	08527	07288	1																															
7290	08528	07289	1																															
7291	08529	07290	1																															
7292	08530	07291	1																															
7293	08531	07292	1																															

[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK							
7366	08606	07365	1																																														
7367	08607	07366	1																																														
7368	08608	07367	1																																														
7369	08609	07368	1																																														
7370	08610	07369	1																																														
7371	08611	07370	1																																														
7372	08612	07371	1																																														
7373	08613	07372	1																																														
7374	08614	07373	1																																														
7375	08615	07374	1																																														
7376	08616	07375	1																																														
7377	08617	07376	1																																														
7378	08618	07377	1																																														
7379	08619	07378	1																																														
7380	08620	07379	1																																														
7381	08621	07380	1																																														
7382	08622	07381	1																																														
7383	08623	07382																																															

[illegible]

[illegible]



[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7510	08751	07509	1																														
7511	08752	07510	1																														
7512	08753	07511	1																														
7513	08754	07512	1																														
7514	08755	07513	1																														
7515	08756	07514	1																														
7516	08757	07515	1																														
7517	08758	07516	1																														
7518	08759	07517	1																														
7519	08760	07518	1																														
7520	08761	07519	1																														
7521	08762	07520	1																														
7522	08763	07521	1																														
7523	08764	07522	1																														
7524	08765	07523	1																														
7525	08766	07524	1																														
7526	08768	07525	1																														
7527	08769	07526	1																														
7528	08770	07527	1																														
7529	08771	07528	1																														
7530	08772	07529	1																														
7531	08773	07530	1																														
7532	08774	07531	1																														
7533	08775	07532	1																														
7534	08777	07533	1																														
7535	08778	07534	1																														
7536	08779	07535	1																														
7537	08780	07536	1																														
7538	08781	07537	1																														
7539	08782	07538	1																														
7540	08783	07539	1																														
7541	08785	07540	1																														
7542	08786	07541	1																														
7543	08787	07542	1																														
7544	08788	07543	1																														
7545	08789	07544	1																														

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7582	08827	07581	1																														
7583	08828	07582	1																														
7584	08829	07583	1																														
7585	08830	07584	1																														
7586	08831	07585	4																														
7587	08832	07586	1																														
7588	08833	07587	1																														
7589	08834	07588	1																														
7590	08835	07589	1																														
7591	08836	07590	1																														
7592	08837	07591	1																														
7593	08838	07592	1																														
7594	08839	07593	1																														
7595	08840	07594	1																														
7596	08841	07595	1																														
7597	08842	07596	1																														
7598	08843	07597	1																														
7599	08844	07598	1																														
7600	08845	07599	1																														
7601	08846	07600	1																														
7602	08848	07601	1																														
7603	08849	07602	1																														
7604	08850	07603	1																														
7605	08851	07604	1																														
7606	08852	07605	1																														
7607	08853	07606	1																														
7608	08854	07607	1																														
7609	08855	07608	2																														
7610	08856	07609	1																														
7611	08857	07610	1																														
7612	08858	07611	2																														
7613	08859	07612	1																														
7614	08860	07613	1																														
7615	08861	07614	1																														
7616	08862	07615	1																														
7617	08863	07616	1																														

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7618	08864	07617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	X68742	94.1	101	1	263	3453
7619	08865	07618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7620	08866	07619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7621	08867	07620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7622	08868	07621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7623	08869	07622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7624	08870	07623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7625	08871	07624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M23613	94.8	290	83	966	1296
7626	08872	07625	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7627	08873	07626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7628	08874	07627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7629	08875	07628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7630	08876	07629	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7631	08877	07630	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7632	08878	07631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7633	08879	07632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7634	08880	07633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7635	08881	07634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7636	08882	07635	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7637	08883	07636	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7638	08884	07637	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7639	08885	07638	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0						
7640	08886	07639	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0						
7641	08887	07640	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7642	08888	07641	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7643	08889	07642	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7644	08890	07643	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7645	08891	07644	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7646	08892	07645	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7647	08893	07646	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7648	08894	07647	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7649	08895	07648	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7650	08896	07649	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7651	08897	07650	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7652	08898	07651	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0											

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7654	08900	07653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7655	08901	07654	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7656	08902	07655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7657	08903	07656	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7658	08904	07657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7659	08905	07658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7660	08906	07659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7661	08908	07660	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7662	08909	07661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7663	08910	07662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7664	08912	07663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7665	08913	07664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7666	08914	07665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0M4810	97.2	71	1	2201	2284
7667	08915	07666	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7668	08916	07667	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7669	08917	07668	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7670	08919	07669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7671	08920	07670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7672	08921	07671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7673	08922	07672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0X69910	99.6	236	1	1840	2910
7674	08923	07673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7675	08924	07674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7676	08925	07675	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7677	08926	07676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7678	08927	07677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7679	08928	07678	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7680	08929	07679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7681	08930	07680	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7682	08931	07681	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7683	08932	07682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7684	08933	07683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7685	08934	07684	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7686	08935	07685	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7687	08936	07686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7688	08937	07687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7689	08938	07688	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						

[illegible]

[illegible]



[illegible]

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7834	09083	07833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7835	09084	07834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7836	09085	07835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X56976	92 287	1	3066	3419
7837	09086	07836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7838	09087	07837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					

Table 219



EP 0 679 716 A1

CCTTTTNCCT CTTACTTGAA GGCAGAATCG CAAAACGTTT GANATGGCTT TCCTAAACTA 300  
CTCTACTCTG GTGNGAGCTC ATTTACCACA NGAAGCCTTA TAACACCGTT TNN 353

5 SEQ ID NO:7746  
SEQUENCE LENGTH:327  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS08996  
SEQUENCE DESCRIPTION:  
GATCAGGTGA TTGCCTTTCT CAGCTGTCAG TTCTCTAATT TCAGGCTTGG TAGCTTGTAG 60  
GAACTGAAAT TGCAATTAAA ACCTTTATAA ACTCAAACTA AATCATGAAT TACAGAAAAA 120  
GTCCATTCTT CCAAACTTG ATGTTACCAC ACTTACAAGT TTAAAAATATG AAGTCGACTG 180  
15 TTAAAGGAT TCTGCATATA TTCTAGTGTG CACATTCAGA AACATTTTTC TTGGAAAAAG 240  
TACCCAACAT TTTTATAAC TGCACATATT AATTTATTGC CAGAATAAAT TGCATTGCAT 300  
GCTAAATTAA NGTCAGATAN TTCNAAA 327

20 SEQ ID NO:7747  
SEQUENCE LENGTH:153  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08997  
25 SEQUENCE DESCRIPTION:  
GATCATGTAA ACTTGCTGTT TTNGTTTTN CCTGCCGGGT GTTGATGTG TGGTGACTTG 60  
CGGATTTATG TTTCAGTGTA CTGGAACTT TCCATTTTAT TCAAGAAATC TGTTCATGTT 120  
AAAAGCCTTG ATTAAGAGG AAGTTTTTAT AAA 153

30 SEQ ID NO:7748  
SEQUENCE LENGTH:41  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS08998  
SEQUENCE DESCRIPTION:  
GATCTTAATT TTGTTTTTGG TTAAAAATAG TGTTTCCTTT N 41

40 SEQ ID NO:7749  
SEQUENCE LENGTH:299  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08999  
45 SEQUENCE DESCRIPTION:  
GATCTATCTA AATGCCGATT TGAGTTCGCG AACTATGTA CTGCGTTTTT AATTCTTGTA 60  
TTNANACTAT TTAATCCTTT CTAATTGTCG CTAAATATAA TTGTTTTAGT CTTATGGCAT 120  
GATGATAGCA TATGTGTTCA GGTTTATAGC TGTTGTGTTT AAAANTTGAA AAAAGTGGAA 180  
50 ANCATCTTTG TNCATTTAAG TCTGTATTAT AATAAGCAA ANGNTTGTNT GTATGTNTGT 240  
TTNATATAAC ATGACAGGCA CTAGGACGTC TGCCTTTTTN NGGCAGTNCC GTTAAGGGN 299

55



5       SEQ ID NO:7844  
        SEQUENCE LENGTH:37  
        SEQUENCE TYPE:nucleic acid  
        STRANDEDNESS:single  
        TOPOLOGY:linear  
        SEQUENCE DESCRIPTION:  
        CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

10       SEQ ID NO:7845  
        SEQUENCE LENGTH:37  
        SEQUENCE TYPE:nucleic acid  
        STRANDEDNESS:single  
 15       TOPOLOGY:linear  
        SEQUENCE DESCRIPTION:  
        CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

20       SEQ ID NO:7846  
        SEQUENCE LENGTH:38  
        SEQUENCE TYPE:nucleic acid  
        STRANDEDNESS:single  
        TOPOLOGY:linear  
 25       SEQUENCE DESCRIPTION:  
        CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

30       SEQ ID NO:7847  
        SEQUENCE LENGTH:22  
        SEQUENCE TYPE:nucleic acid  
        STRANDEDNESS:single  
 35       TOPOLOGY:linear  
        SEQUENCE DESCRIPTION:  
        CCAGGGTTTT CCCAGTCACG AC 22

40       SEQ ID NO:7848  
        SEQUENCE LENGTH:22  
        SEQUENCE TYPE:nucleic acid  
        STRANDEDNESS:single  
        TOPOLOGY:linear  
 45       SEQUENCE DESCRIPTION:  
        TCACACAGGA AACAGCTATG AC 22

# 50   **Claims**

- 55   1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA , a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.



Fig. 1

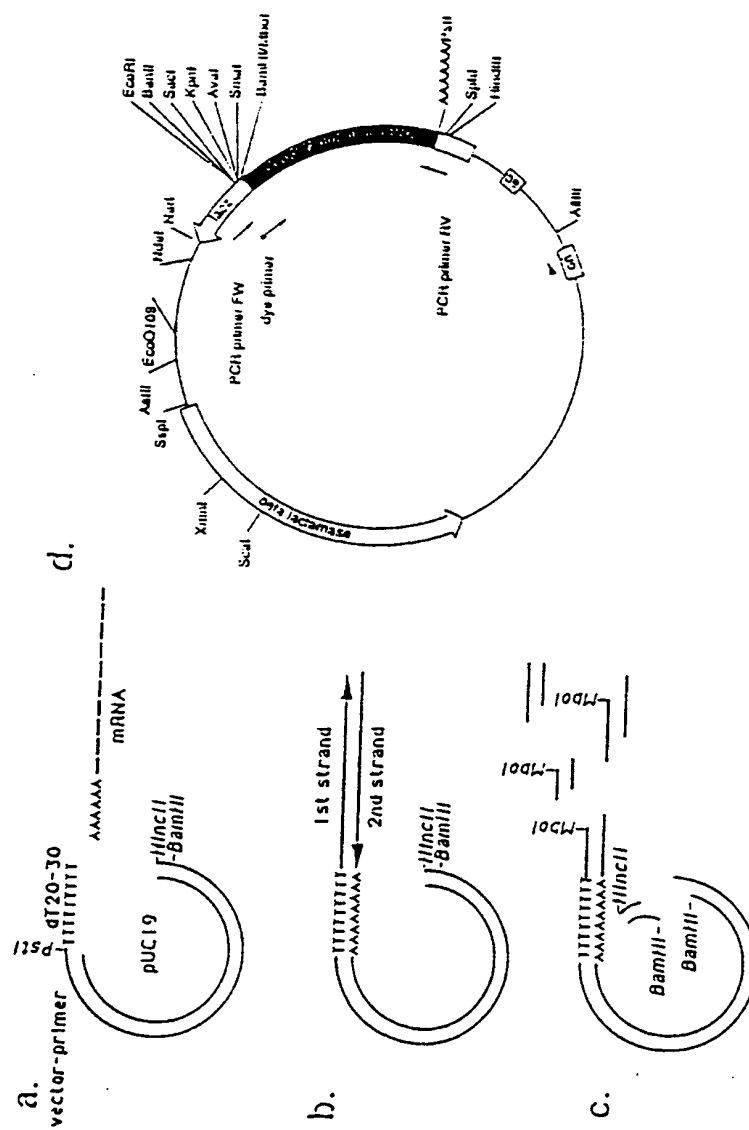


Fig. 2

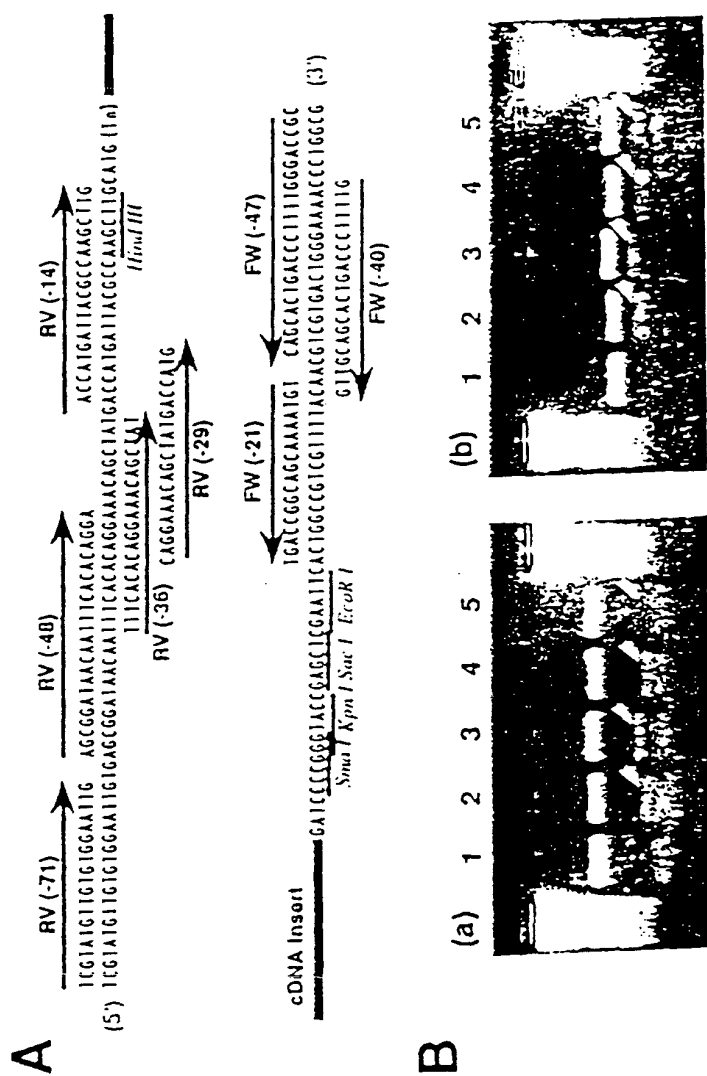


Fig. 3

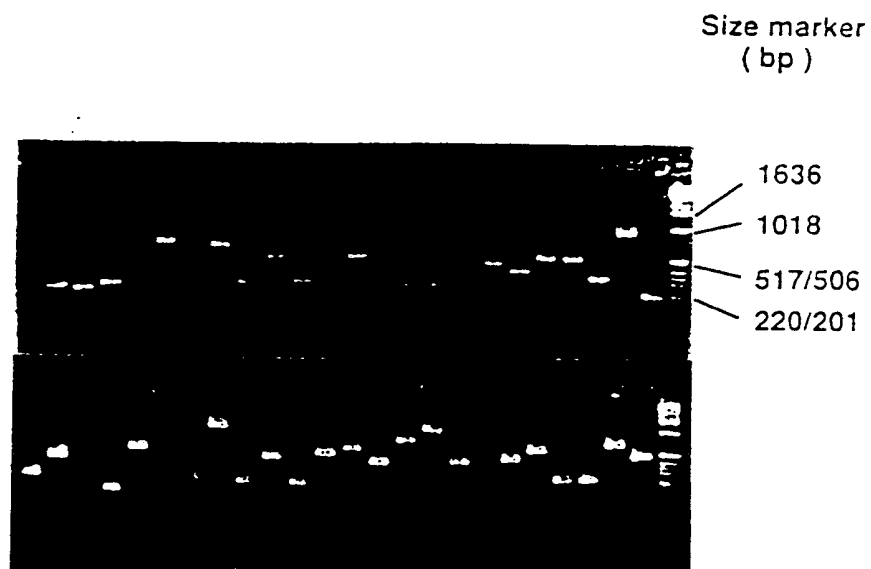


Fig. 4

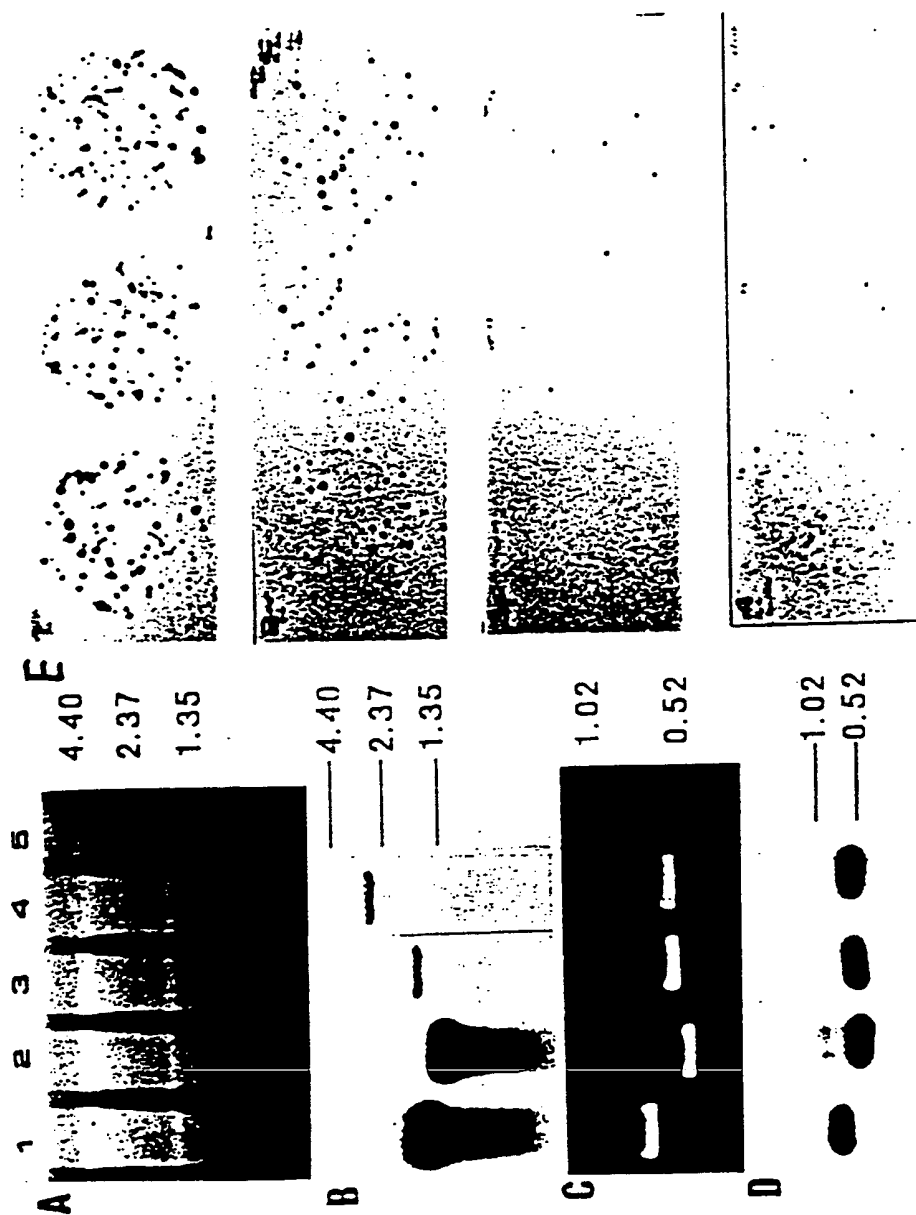


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- $\alpha$	$\alpha$ 1-andrypsin	HnRNP core protein A1	Inter- $\alpha$ -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b)x10	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library				
Group	Clone	Gene	A in 902 (%)	B "in 0,800 (%)" C "in 26,400 (%)"
I	a15	Elongation factor - 1A $\alpha$	22 (2.2)	307 (3.5) NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0) NT
	1b038	$\alpha$ -1-antitrypsin	8 (0.8)	119 (1.4) NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7) NT
	c13a04	NADP(II) Menadione oxidoreductase	4 (0.4)	27 (0.3) NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3) NT
	1b042	Human RNP core protein A1	2 (0.2)	7 (0.1) NT
	s155	unknown	1	5 (0.02)
	s159	unknown	1	4 (0.02)
	s639	unknown	1	3 (0.01)
II	s635	unknown	1	2 (0.01)
	s170	unknown	1	1 (0.004)
	s154	unknown	1	1 (0.004)
	s167	unknown	1	1 (0.004)
	s645	unknown	1	1 (0.004)
	s647	unknown	1	0 (<0.004)
	s632	unknown	1	0 (<0.004)
	s155	unknown	1	5 (0.02)
	s159	unknown	1	4 (0.02)
	s639	unknown	1	3 (0.01)

Fig. 6

GS	CII	Chromosomal position	Sequences of primers		AT	IIQ	IIE	LIO	CO	G	T
			Sense	Anti-sense							
9100788	pin2366	1	CAGAGCCCGTAGCAACTAT	AAGTTATGTGCGGTACAG	48	114	115	104	110	1	2
91001026	pin2444	1	AATGGGACGTACACTGTA	CCAGCTTCCTGCATCTGAGA	48	83	91	>200	>200	1	1
91001075	pin0883	1	TGGACTGGATACCTATCT	ACAAGTACCCTGAATGGCT	48	124	124	103	107	4	4
91001087	pin1772	1	GTCACTCTGAGCCATAGCAC	ACCATCTCAGCCGACACTT	50	104	104	180	>200	6	6
91001094	pin0347	1	GCCGCTAACAGAGGAAGTC	TAATTTCCCATCCCGTAAC	51	114	116	>200	200	1	1
91001116	pin1771	1	GGGTTTCAATAGGGGTAGACC	GCCCAATCTGTCAAACTG	49	95	95	78	107	1	1
91001191	pin0609	1	TTGCTGGATTGAACCTTTG	GGCTGAACATTCACCTCTTG	47	97	97	-	200	1	1
91001200	pin1351	1	TTAAGAGACCCCTATGGAGACC	AATATCTGGTAGTCACCTAC	47	97	98	-	-	1	1
91001316	pin0982	1	TCAGGTCTGCTGGAGGATG	AACTCACGACAGATATTTG	53	120	122	>200	>200	1	1
91001416	pin1518	1	AAGGTGTACAGGATATTTGCAGA	TGCAATAGCCCAATCTCAT	47	130	125	>200	>200	1	1
91001439	pin1439	1	CCMAAGACCTCGGTTGACAA	TTTGGGAGAGCCATAGACAG	51	100	100	>200	-	1	1
91001464	pin0427	1	TACTCAGTGGAAAGATAAAC	CAGTGGACCCACATTTCTTA	40	98	98	-	-	2	2
91001468	pin2785	1	CCCAATCAATTTGTTAAATG	TTTGAATCAGACATGAAGTT	43	102,175	100	>200	>200	1	1
91001554	pin2291	1	CCAGAGAGTTCAGAGGATG	GGTACAAAGTGCMAATGACT	46	57	57	78	155	1	1
91001572	pin2006	1	CCACAATGCTAGCAGTGT	AACCTTATTCGAGCTCTT	44	58	58	>200	>200	4	4
91001620	pin1350	2	CATGATCTCTGGGTGGTA	AACAGTAGTCCGAGCAAT	46	84	108	-	-	1	1
91001636	pin1730	2	AGGCTGAATGTGGCATGCT	CCCGTTATTGCTACATGCT	48	119	119	93	115	1	1
91001681	pin0931	2	AAGCCATACAAATACCAA	TTCMAATGTTTACCAGTA	40	90	90	-	-	1	1
91001690	pin0925	2	TAATGTACCAAGATGAATAG	TAATGTAATAATGGAGTAA	45	88	88	-	-	1	1
91001713	pin2010	2	CCAGATGGAAGGAGAGTCT	CTGGAAATAGGAGATCAACAG	47	125	125	150	>200	1	1
91001732	pin0935	2	TGGATTTTGTCTCTAATA	GGAAATATCGCTTCAGTTG	43	103	103	-	-	1	1
91001768	pin2093	2	AGTCCTCTTGGCTCCTCAT	TATGTCAGTGGCTTTATTG	52	137	137	>200	-	1	1
91001784	pin2435	2	TTTGTACCTACGTAGAGTACT	ATCGTCCACACATAGTGA	45	105	108	-	-	1	2
91001791	pin1671	2	TTATTAGGAGATCATTTCTGTG	AGTCCCATTCCTCCACATG	45	67	65	>200	>200	1	2
91001843	pin1245	2	TTGCTTCCCGTCTAAGT	ATGTACAAATTCGGTATGTAGG	45	75	75	170	190	1	1
91001855	pin1246	2	ATCTACTGTTTGTGAAGTG	ACTGATTTTGGTCCCATCTG	44	68	67	-	-	1	1
91001875	pin0449	3	CGAACATTTACAGCTGCATA	ATGATTATTAGGACGGA	43	68	68	-	-	3	6
91001901	pin1758	3	TCTGGCTCTTTGGTGTGGA	GGCCCACTGACTACAATGTC	51	115	115	-	-	1	1
91001918	pin2434	3	AAGAAGACACACTGCCTAA	ATGTATAGCAAAATCCAAAG	42	90	90	-	-	1	1
91001919	pin0668	3	GTAGTCTCTGCCCTTTAGC	AGGATTGATTCTTCACT	43	77	77	-	-	1	1
91001977	pin1729	3	GGTCTGTTTATTGACAT	AACAAGAGGATGTTTCAGA	43	75	75	155	>200	1	1
91001986	pin1022	3	GATCCTGGTGTGATGTCAGTC	CTGCCAAATACAGGAATCAT	46	83	83	160	140	1	1
91001996	pin2209	3	ACCCAGTCCCAATCCAGT	ACACTCCCCAGGCCCTTACT	55	105	105	113	>200	1	1
91001998	pin2455	3	ATCTAGCTGCTGATGAT	TTAAGAGATGAATTTATTTGTT	42	110	110	130	130	1	1
91002071	pin1252	4	GTCTTTGCTATCTGTGTTA	AAGCAATTTATTTGAGGCTTAA	43	90	90	95	>200	1	3

Fig. 7

g10004148	pm12356	4	GGCCAGTTTCTCTAGTAT	GTCAGTTTATTCAGAGCA	42	62	62	>200	69	1	2
g1001052	pm1151	4	GTGCCATGCACGTGTTAT	GTCAATATTCATCATCA	43	80	80	-	-	1	1
g1001215	pm1988	4	AGAAATTAATAGCATAGGT	TAGAGTCAAGTTCCTGTG	43	100	100	130	-	1	1
g1001298	pm2367	4	ATCAAGTTTAAATGTTCA	CATCCATCACAACAGTC	43	116	116	>200	180	1	1
g1000993	pm1901	5	TCTCGTGAAGAGCAGCACA	TCTAAGGAGCAACAGCATC	49	101	102	113	200	1	1
g1000998	pm1809	5	AGCAATGCGTTATCCACAG	CTAAGAGCTGACCCCTTCAT	45	87	87	>200	>200	1	1
g1001065	pm1319	5	TCACCCAGATAATTTACAGT	GAGACATAGCAGGTAGAT	44	120	120	-	-	1	1
g1001101	pm2364	5	TTACCTTACCGTGTCTTAC	AGCAATATCCCAAAAGC	47	89	89	100	>200	1	1
g1001461	pm1160	5	ATTGTGAGTGGTTTACTA	AGAAATGGATGCTTTATTC	43	101	99	>200	>200	1	1
g1000353	pm2720	8	AATGTCATAGTCTCTTCA	TGCATCCTCAATGCTCTCT	44	78	78	72	>200	2	3
g1001326	pm1154	6	CATTGACAGACAGCAACAG	CCTGGCCCTCTCTCTGAGTA	53	102	104	145	200	1	1
g1001434	pm1216	8	TAGGCAAAACACAGAGAGAG	AGGAGCTGGTGCAGGTC	48	65	65	110	>200	1	1
g1001457	pm1785	6	TATATCAAAATTCCAAGTCTG	TCTAATATTCGGTCCCTATCT	46	90	>200	>200	>200	1	1
g1001523	pm2285	8	TTGTACGTTGTGCTCAGT	TTTAAATGTCAAGTAT	42	86	70	>200	100	1	1
g1001525	pm2328	6	GCACCTAAGCCTCCCAAGT	TTTATATCAGTCCAAAGC	49	138	138	>200	>200	1	1
g1001582	pm2610	8	TCTGCATTCAGAGAGCAGC	TTTGAGATTTTATGATCATTC	43	62	62	>200	45	1	1
g1000624	pm2091	7	GACCTGAAGTGTGAATGAT	AAGTACCTTTATGGATTT	45	119	119	>200	-	1	2
g1001145	pm2281	7	AGCCAACTCGGGTCACTCT	CCAGGGACAGGTGAGTCAT	56	159	159	155	>200	4	4
g1001469	pm2219	7	AATCATTTGCCGAGACTGTA	AAGACAACCTTATCCAGACA	45	88	89	130	-	1	1
g1001579	pm1102	7	TCAGGCAGCTGCTCAGATA	TTTCCAGGTTAATCTGTTA	44	77	76	170	-	1	1
g1001207	pm2956	8	AACAGTATTCGCTGTGTCAGACTAG	TCCATTAATAGGCCAGCTTCAG	47	81	81	105	70	1	1
g1001176	pm2527	9	TTCCTCTAATGGTGTCTAC	AAAACCAAACACACTAAG	48	99	99	118	180	1	1
g1000260	pm2708	9	TGTATTCGATTTGGATTCTC	CAAAAGCAACAGCAGATA	44	95	95	-	85	1	1
g1001055	pm2995	97	TTGCCATCAACACATACA	CTGTGAGTTTGTGTTCTG	43	55	55	-	-	1	1
g1001157	pm2959	97	TTAAGAAATCAGCCCTCATG	CACATGCTATTTGACACT	44	74	74	72	73	1	1
g1001288	pm2547	10	AAGTATTCGCAAGATGTA	AAGAAACAGCTGCTTGCG	45	138	139	>200	>200	2	3
g1001264	pm2245	10	TGTGAATGCTATCTCTCT	GGATGCTTCCATATCAGT	47	100	100	200	>200	1	1
g1000724	pm2664	11	ATCAAAACAACANTCCAGA	ACTATATATCTGCCAAGT	42	117	121	134	95	2	2
g1001159	pm2880	11	GAATAGCTTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	84	95	1	1
g1001315	pm2445	11	AAAGTGACCTTGAATGGACAGTGG	TGGAGCCAAATATACCTGCTACT	50	153	153	>200	160	1	2
g1001352	pm2943	11	AGGGTGAAGGGTATTTTAGG	CACATCATGCTGAGAGCTA	47	83	85	-	-	2	2
g1001469	pm2559	11	AACCTCTAGTAAAGGCAATG	TTATTAAGCAATCCAGTA	37	47	47	125	53	1	1
g1001570	pm2810	11	CTGTAAGGTTTGGCAATTAGT	TTTCATTTTCTACCAGATTAT	42	75,82	75	145	>200	3	3
g1000279	pm2266	12	AGTGTATGGAAGAGCTTGAG	GTTCATTTGAACGGGTAGC	48	130	130	103	>200	1	2
g1001163	pm2756	12	TCTCCCTATCACACCAGT	AATGATTTCGATAGGACA	49	88	89	>200	120	1	2
g1001193	pm1193	12	CACAGATAAAGAAATCATA	ACCTAATTTAGTTTCTCAC	46	100	100	-	-	1	1
g1001235	pm2790	12	CATCATGTACAGTCAGAG	CAGTTTGTCAAAATGATTG	44	83	82	93	87	1	1
g1001274	pm1355	12	ATGTCAGTATGCTCTCATGG	GAGACAGAGTAAAGCAACAC	47	87	87	>200	>200	1	1
g1001308	pm2668	12	CCAAAGTGTGGGTACAG	TTCAATAGACCTTGGTTAC	47	95,165	95	>200	>200	1	1
g1000159	pm2645	13	CTAAGATTTAATGCGATCC	AGTTAGTGTATGGCAGAGGA	46	104	104	>200	-	1	2



Fig. 8

91001014	pml1659	13	TTGTAAAGCTATCAGAGTCA	AGACAGACTATGCCATCTA	44	109	200	109	>200	100	1	1
91001290	pml1731	13	GCCTCTCCGTGCTGTGGT	GCAGTAACTAGCTATCTCC	50	122	122	>200	>200	130	1	1
91001362	pml1118	13	ACTGAAATGACATAGTCT	TACATTAACATGACATTGTGA	40	61	61	95	103	1	1	1
91001366	pml0364	13	TGCTAGCTTCCCTCCTTA	GAGCATTTCTGTGTCCTA	45	67	67	-	-	-	1	1
91001389	pml2301	13	CATGAACCTGCTCAGCACA	GCCTAACITTAATGCTGACC	51	100	100	100	>200	-	1	1
91001492	pml0541	13	AAATGAATGTAATAGCACT	ATTAGTTACAGGGAGAT	41	72	72	-	74	1	1	1
91001367	pml0441	14	GTTTAAGTTTGAATTGGG	CATCCAGCTTACATTTCT	41	77	77	>200	180	3	4	1
91001564	pml2307	14	CGTCTAACTCTGAATC	AATGTCATTATCTCAG	42	55	55	>200	>200	1	1	1
91001576	pml2019	14	ATCACAATACCTTAGTTG	ACGAACTTTATGGAGAT	39	69	69	-	-	1	1	1
91001339	pml2220	15	TCCCATCTCTCAGTTGAAT	TGAGAACAAAAGAACAGT	47	70	70	80	150	1	1	1
91000980	pml0985	16	TTGGATGGAAACCTTGCTA	ACTATGGCCCTGAATGG	48	79	79	65	70	2	2	2
91001242	pml1127	16	CCCTGTTTATACATGTC	TATTAAATGTCCTTTCAT	44	105	105	103	102	2	2	2
91001516	pml2543	16	ACAGTCTAAATCAAGTG	TCTGCAACTCAAGTGCAT	45	70	70	>200	-	1	1	1
91001566	pml0913	16	TTTGTGCGACTATGTAAT	TCACTTTAATGGAAACAG	41	53	53	>200	>200	1	1	1
91000806	pml1157	17	CTCTCAATGTTCTACAG	TAGAGGAGAACTCTGGTT	47	77	77	140	>200	2	3	1
91001015	pml2369	17	ATATCACTTCCCATCCAT	TCAATAGCTCTCTCAAGC	50	80	80	>200	>200	1	1	1
91001156	pml202	17	CAGAAATAGTGCAGCAAT	TGCTATGCTCTTTAAGT	45	103	100	>200	>200	2	2	2
91001173	pml2117	17	AAATCTGTGGTTATTC	GTCATCTACGTGACATGG	41	118	118	145	200	1	1	1
91001301	pml1878	17	TAAATTTGGAAATCTTTGGA	ACACATTTGGGTTTGGTTAAG	47	100	100	95	97	1	1	1
91001316	pml0511	17	TGTGACAGCAGCTTCAT	TCTGACATTTAATCCAGC	45	128	128	-	-	1	1	1
91001356	pml0538	17	CATCTCAGACAGGGAAC	ACCTAAGTCTCAGAGAAC	48	90	90	69	>200	1	1	1
91002212	pml2212	17	TGACTGCAATAAGGAGTTGT	GACATACCACTTTATTCT	46	90	90	180	>200	1	1	1
9100142	pml0642	17	GTCTCAGCAGATTTCAGGT	ACTTCTCTGTGAGACACA	45	68	68	68	160	1	1	1
91001815	pml1815	19	TGTGTTCTCCAGCTTTGTAG	GTTACATGCTCTGGTACAG	48	65	65	>200	>200	1	1	1
91001417	pml0289	19	GGATCAGACCAACAGTCTG	GCAAGGTATAACAGATTA	46	50	50	-	-	1	1	1
91001467	pml1609	19	GAAGCCCAACCTGCACCTCA	GGAGAGTATTGGGACGGT	54	93	93	>200	>200	2	2	2
91001879	pml1879	20	GCCA TGCTGTAAAGTGATGT	TTAGAGGCATTAGTAGGATA	48	140	140	-	-	1	1	1
91001146	pml1146	20	GCCCTAGGATCACTGCTC	ACCACCAAGTCTTTCAGG	52	66	66	180	>200	1	1	1
9100112	pml0112	20	TGCTGTAGTACGTCTACAG	TCCCTATCATGGCTGTGT	49	59	59	59,115	59	1	1	1
9100332	pml0332	20	CTGCTGGCTAGTCTGACTC	CAATGCTTAGAGGAGCAT	49	135	135	153	160	1	1	1
91001647	pml0647	20	TCTGAATGATGTGGAAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	-	-	1	1	1
91001158	pml1774	20	GGAGCCACATGGATGATTG	AAATGACCCCTGGCACCTC	52	124	124	>200	>200	1	1	1
91001210	pml1235	20	AGCCATCTGGTTATGTTTA	GGAGGAGAAATGAACCTCAC	44	90	90	>200	>200	1	1	1
91001377	pml1701	20	TCCA TGGTGTAGAACCCAG	CCACATCTCCACAGGGAGT	54	142	142	>200	74	1	1	1
91001385	pml2101	21	GTCAAGCTCAATGCTACACAG	TTTATGTCGACACAGAGT	45	130	130	180	>200	1	2	1
91001427	pml0648	21	CTTCTGCTAATAAGTAGAG	ACATTTGTTCACTAAATGA	38	58	58	145	>200	1	1	1
91000976	pml0912	22	GGTGTAGTGAACCACTTGT	AGTGCACCATCTCCTGTC	46	124	124	>200	>200	1	1	1
91001444	pml0911	22	GGTCTGTTCTCCCATCTGT	AGAAAGCCCAAGTAGTCC	48	65,80	65	100	125	1	2	1
91001473	pml2231	22	TGAGCTGCACCTACCTGTGAGAG	AAGCAGGTGAGTTGGGTTTCT	50	94	94	67	135	2	4	1
91001479	pml2328	22	TACAGCCCTCCAGCTAAC	TTTATCTGCATCCACTACAA	46	65	65	190	>200	1	1	1

Fig. 9

g1-000999	pml1759	X	CTGCCATGTTACCTGGATT	TCCCCAGCACATATTAGCA	47	103	-	-	-	1	1
g1-001149	pml2180	X	GGAGGGAGATATAGATTGT	AAAAATCCAGAGACGTA	48	70	135	150	-	1	1
g1-001161	pml0608	X	TTCATAAGTGTACACAGT	GGAGGATTGAGATACACAT	40	85	85	>200	71	1	1
g1-001106	pml1294	X	TAATGCCAGTGAATGTGCGTAA	GTAAGGTATTCCTTGGCATCAGA	47	82	82	>200	80	2	3
g1-001136	pml2269	1,10	ATCCTGCTGAATACATCTG	GGGAGAGACATACATGAC	46	70	68	130	-	1	1
g1-001104	pml0112	1,2,12,13,Y	GATCCGATGGGAGTGTAAAT	AATACAAAGCTAACCCACA	44	69	60	170	-	1	1
g1-000303	pml2272	1,2,3,5,8,12,14,17,X	TTCGAATGCACATTCTCTAT	TTATTTGTAGCAAGCACT	43	130	130	150	132	2	2
g1-001140	pml0314	1,2,4,5,8,16	TATCAGCTGGAATGTGCAC	TTACGTATCCAGCCACCA	45	93	93	110	-	1	3
g1-000303	pml1481	1,2,6,X	TCCAAATGAAGAGGTGTAA	AGTTCAGACCCAGGTGAATG	49	96	96	100	100	1	3
g1-001154	pml1561	2,20,21,22	GTCTGTACGCCAGATTCGA	TTTATTTGTGCTCCAAAGT	43	110	110	170	150	1	1
g1-000326	pml2785	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATCTGGACT	TTATATGGTTGTACATCG	43	81	81	-	-	2	6
g1-001077	pml0943	2,5,14,C	GCCTTGTATTCCACACTC	ATCCCTTTGCTCCAGTAA	46	82	82	>200	82	1	1
g1-001192	pml1853	2,8,12	TCTGAGGACATCCAGACAG	CAGTCAAAACACACGGTAT	49	95	95	93	160	1	1
g1-000919	pml1778	2,9,13,17,X	TGCATAAAGGGAAGACCA	CCGTGTAGGTGTGAAATG	49	78	80	>200	>200	1	2
g1-000109	pml0457	3,10,15	GTCAATTGTATCCAAATTC	ACATTTATTTTTCACGG	37	45	45	-	-	1	2
g1-000071	pml2851	20,X	CATGTACTCAGAGCACTTC	GATTTANCCCATTAGGAAC	50	101	101	101	88	3	3
g1-001426	pml2832	3,6	CAGGACCTGGAGCAGGAAG	ATAGTATGGGTGTGACACAGT	43	80	80	>200	120	1	1
g1-001391	pml1133	3,8	TGGATTGCTTTACCTGT	ACACCTCAGGAGATGTAC	47	93	93	95	>200	1	1
g1-000605	pml2250	3,9,10,15	GCATACAGCCCAATCAGA	CTCTTACACCAAGACAG	50	96	96	>200	125	2	10
g1-001312	pml0626	4,6	GGATTCTATTGCTGTCT	GTATTTGACGGCATTTAC	44	105	100	>200	>200	2	4
g1-001357	pml0608	7,18	AGATCTAATCTATTAGGATA	TTTATAGACATACAGAGGAGT	44	110	110	105	107	1	1
g1-001261	pml253	9,11	CCAGACTACGGCTATGGC	CCCTTACCCAGCAACTCT	55	75,130	75	>200	>200	1	1
g1-001456	pml0115	9,11	AGCAATGTCTACGCTCTAAATA	CCCATATAGTGAAGGTAGTTTC	48	125,155	127	125	>200	1	1
g1-000290	pml0428	10,15,22	ATACCACTCCGCTGTACGG	TTCATTTATTTGATAGTGA	46	100	100	170	-	1	1
g1-000314	pml2303	11,11	GCACCAAGACGANTTCCAG	GAGGAGCGTCTACTGCTCT	50	72	74	72	>200	3	20
g1-000103	pml2843	12,19	GATCTCAGTCTCGCTTTAT	TTGGGATGAGAAATAACT	44	83	83	81	-	1	7
g1-001487	pml2725	13,16	ATCTGTGTGCTGCTTTCC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	1	1
g1-000376	pml2780	14,16	AACCTGTTTACCGCATCT	AGGTATTTGTCCACCAGAA	48	87	87	>200	>200	1	1
g1-001393	pml1683	17,20,C	TGTTGGTTTACCATTGAGAC	AGAACACACATCAAGATGC	46	90	90	>200	90	1	1
g1-000356	pml0984	17,C	GAATGTCAATCCAGACGTAG	CTAGTTATCTCTGGCTCTG	44	81	81	>200	200	1	1
g1-001369	pml2217	17,C	TTTATCCCAAGCAAGCAAC	TCTCTCTTCTAGTCTCTC	49	120	120	>200	170	4	11
g1-001140	pml1213	18,C	ACTTAAGTAGCTTTGTACG	TGCTCTCTGGTCTGTAAATA	43	95	95	>200	95	1	1
g1-001217	pml1118	19,20	CCCGAGTTAAAGATTATGT	AGTGAGGTGGAGGATGTA	44	92	92	-	92	1	1
g1-001009	pml2824	19,22	TGCAGAGTGAATTTCCAGAG	CGTAGGTATCTTTTCAGC	46	75	72	160	65	1	1
g1-001172	pml0887	19,22	ATCCCTCTCTCTATTACAC	GCTGTTTAACTACGCTCAC	45	110	110	130	170	2	2
			GCCTGCATCTGTGTGACT	AACCTCTGGGAACAAATCAT	48	91	89	160	86	1	1

Fig. 10

g1001057	pin2049	C	AGGACACAAACACGAGCTAT	TTTCTGATATGACATGAC	45	75	75	101	75	1	1
g1000173	pin1753	M	ATCTCTTTGAGCCATCTCG	GTTAAAGTCTGATGCCATT	42	84	108	64	>200	1	1
g1001056	pin2236	M	GTAGAGCTGCATGATACCC	ACAGACACGGAAATATCAT	42	108	96	110	112	1	1
g1001166	pin0506	M	GTCCACAGTCCAGCCTAAC	GCCACATATAGAAATCCATC	46	74	74	74	>200	1	1
g1001154	pin2354	M	TGCTTTGTGGAGCTCGCT	TTTAACAGTCATTAATACATGTT	44	110	110	110	106	1	1
g1000279	pin2492	M1C	UCTAAGAAAGAGGCACTCA	CTTAAGTCATAGCCAGTGC	46	75	75	75	75	1	1
g1002766	pin2766	M1C	CACAAACAGCAACTTCAG	ATGGTTATTTATCAGATTG	41	83	83	82	83	2	3
g1000285	pin1704	M1C	TCCACCCAGAGAAAGCACT	AAATCATAGGAATAGGTTG	48	75	130	75	75	1	23
g1000318	pin2318	M1C	TGCAAGAGCAAAATCACC	GAACAGGGTAGTCATCG	48	50	50	50	58	1	1
g1000643	pin1689	M1C	CATGAGGCTACGGAAACAGG	AGGAGTCGGTGGTCTTGAG	51	81	84	84	84	4	18
g1000675	pin1442	M1C	AAGCACTCTGAGAGGACA	GAGAGTCGCTTGCTCTTA	49	110	200	110	110	1	9
g1000732	pin1452	M1C	GCAGCAATACCTTACACC	TGGTTCAATTCAGTTCCTTC	51	102	105	102	102	3	13
g1000995	pin0268	M1C	GAAGCTCTGTGAGGAAGT	CAGACCCATCTTTATACC	47	79	79	79	79	3	4
g1001016	pin2703	M1C	ACGATATTAATAGTAGTG	TCAAACTTTAATATAGCT	40	93	93	91	92	1	1
g1001053	pin1144	M1C	AGATGAGTGTGGGTCAAG	CCATTCCTCATTCACAGTT	52	135	140	135	135	1	1
g1001127	pin2290	M1C	ACTGTGATGGAGGTTACA	CCACAGATGACACCGTCT	47	55	55	55	55	1	1
g1001167	pin1626	M1C	TAGTCAGAGATTCAGTAAGT	CTTCCCTTTGGTCTTTCTGT	49	100	100	100	100	1	1
g1001216	pin1240	M1C	AACGTGTTCCATCAGACTG	ACATGTAATTTGATAGTCT	42	110	110	110	110	1	2
g1001253	pin1131	M1C	ACTTAAACCCACAGCAT	ACGAAATAAAGTCCACATCC	48	120	120	120	120	1	1
g1001281	pin0952	M1C	AAGAGAGTTCCCTGCTCA	ACACAGCAGTCAAATAGAA	47	97	97	97	97	1	1
g1001356	pin2216	M1C	ATCTGCATGAGCTAATCT	ATCATGTCAGATGGCAAGGA	51	89	89	89	150	1	1
g1001411	pin0958	M1C	ATGGTTATACAGGGTTTC	CGTCTCTTTTATTTGACAT	45	108	108	108	108	1	1
g1001460	pin2626	M1C	ACATTTAATGGGATGAGTT	GAGACAAAGGCACTCTTA	47	100	77	80	80	1	1
g1001482	pin1210	M1C	TTGTTGACATTCCTTTAGAA	GGACATTTCTAGCCACAGC	51	75	55	75	75	1	2
g1001490	pin0109	M1C	CCCCACAGACATCATCT	CAGTCCTCTGACTGAGACA	46	85	85	85	85	1	2
g1000618	pin2042	No product	CACCAAGTAGCGTGAAGT	TCTTAGTAGTGTCTGTGTG	51	90	90	90	98	1	1
g1000650	pin0304	No product	CTTTGGGATATTTCTCAT	GAATATCTCTGTCATCA	45	87	87	87	87	1	1
g1001254	pin1672	No product	AGCCAGCTCTTTGATGTG	CCCTGGGACTTTTCTATG	43	60	60	62	62	1	2
g1001365	pin2008	No product	TGTGGTATGAATAATCTGA	CTGGATTTGATTTTCTATG	44	87	87	87	112	1	1
g1001373	pin0361	No product	CAGTAGTGTGCTTTGAAATG	TTATGTAATGTGGTTGT	43	88	88	183	>200	1	1
g1001556	pin0819	No product	TACAGCGCTCTTAAAGTC	TTTGAGCATCAGGAATCT	46	82	82	82	150	3	3
g1001574	pin1284	No product	TACATCTCAGACTCATGG	TTTCAAAACTTTATCTT	40	86	86	86	>200	1	1
g1001622	pin1606	No product	ATCAGAGCTCAGTCTGTAG	ATTTGGCTCTGCTGCTGTC	44	57	57	67	67	2	2
g1001640	pin0852	No product	GATCTGAGCCCTAACGGGA	TTTGAGTTTCACTTATTC	45	54	54	54	54	1	1
			GATCTGTGCTCTTTTCACA	TTTATACAGACACCATAC	30	45	45	45	45	1	1

Fig. 11

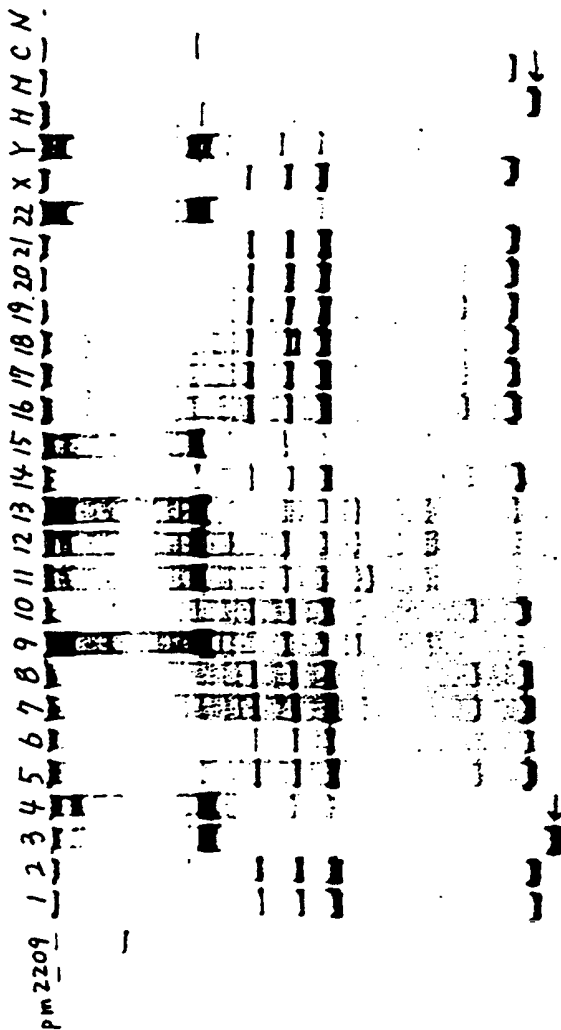


Fig. 12



Fig. 13

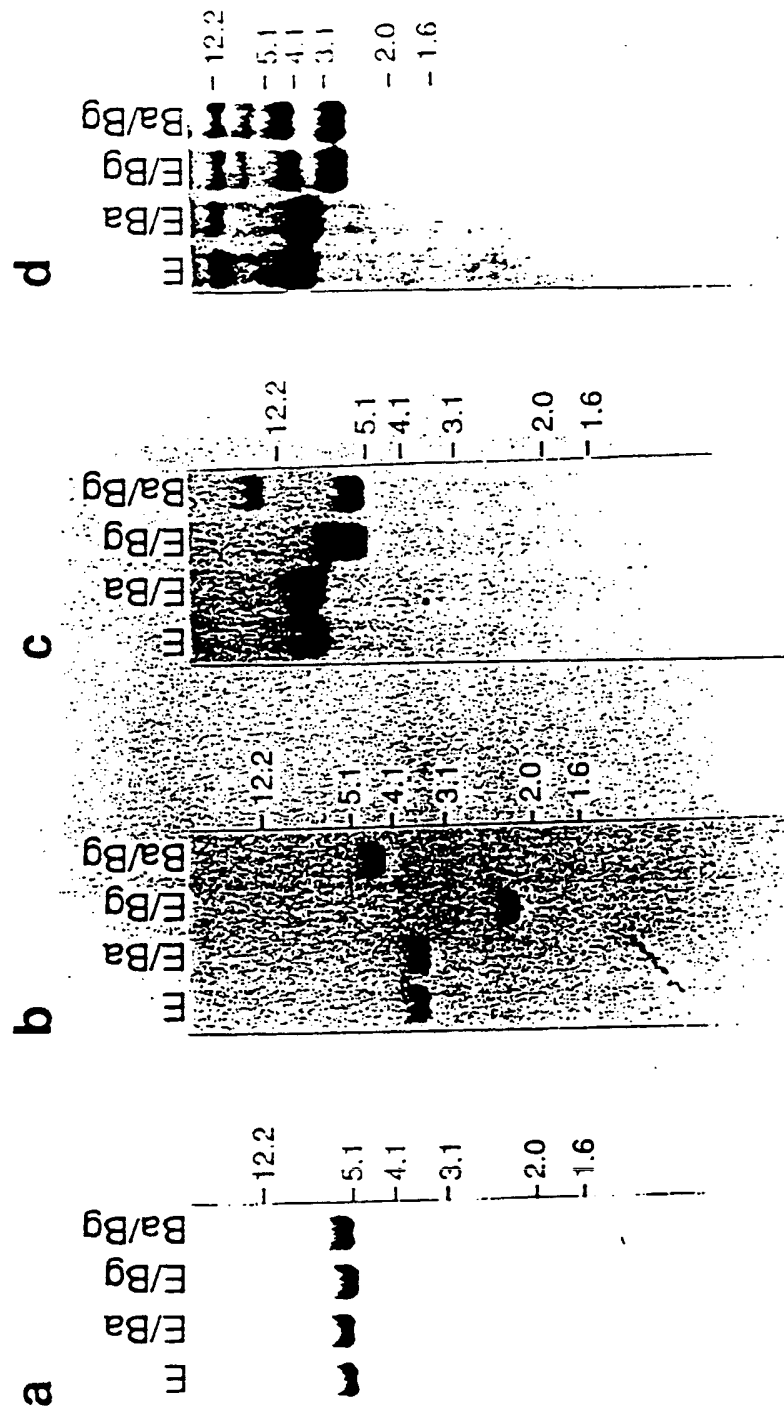


Fig. 14

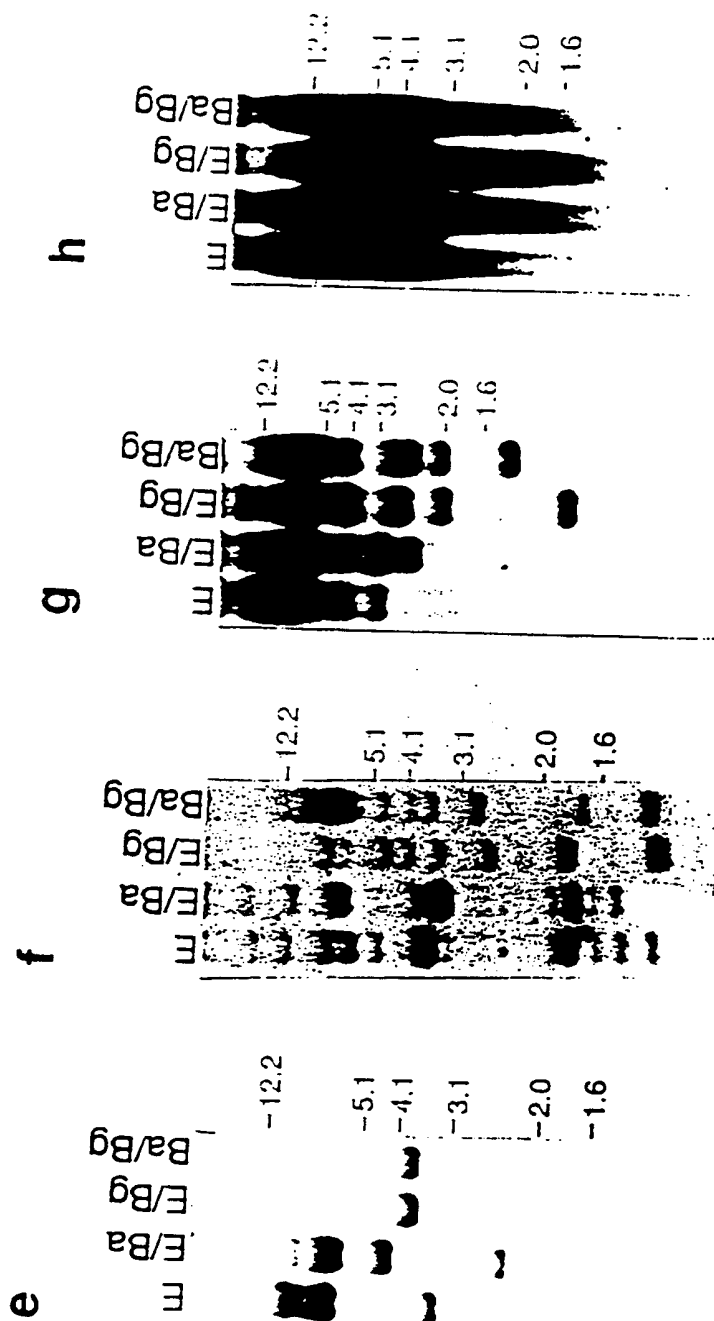


Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (3)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A *	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868 *	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418 *	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9



Fig. 16

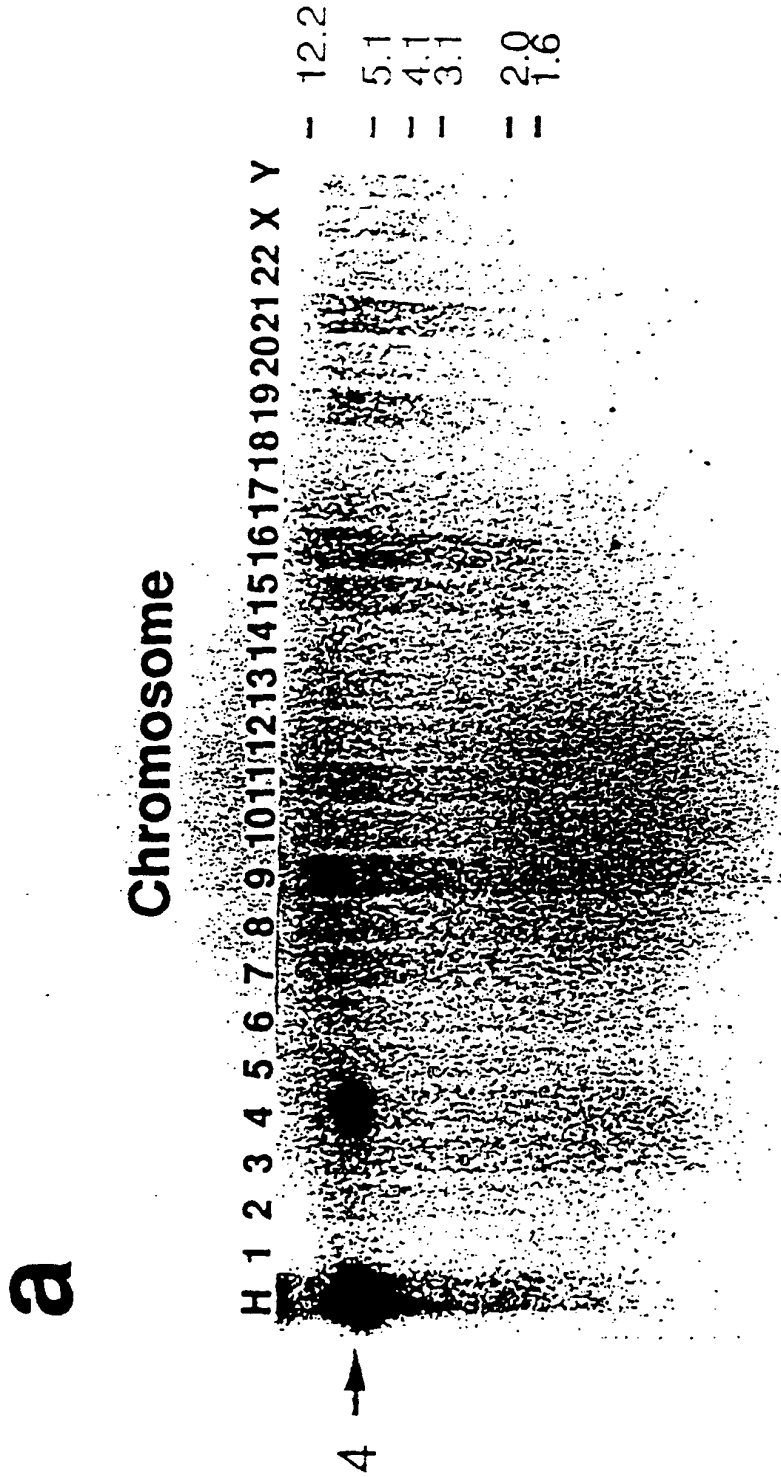


Fig. 17

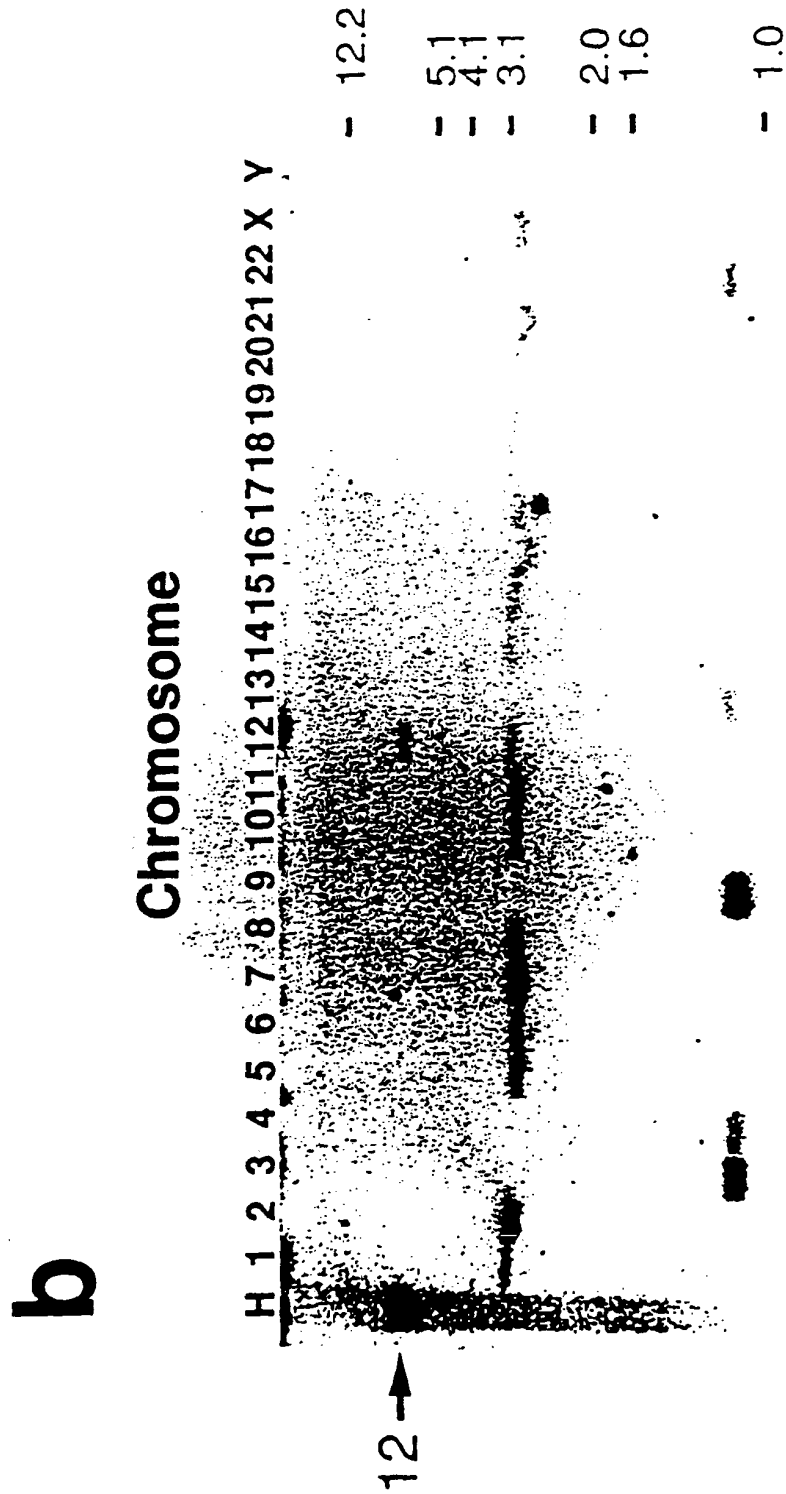


Fig. 16

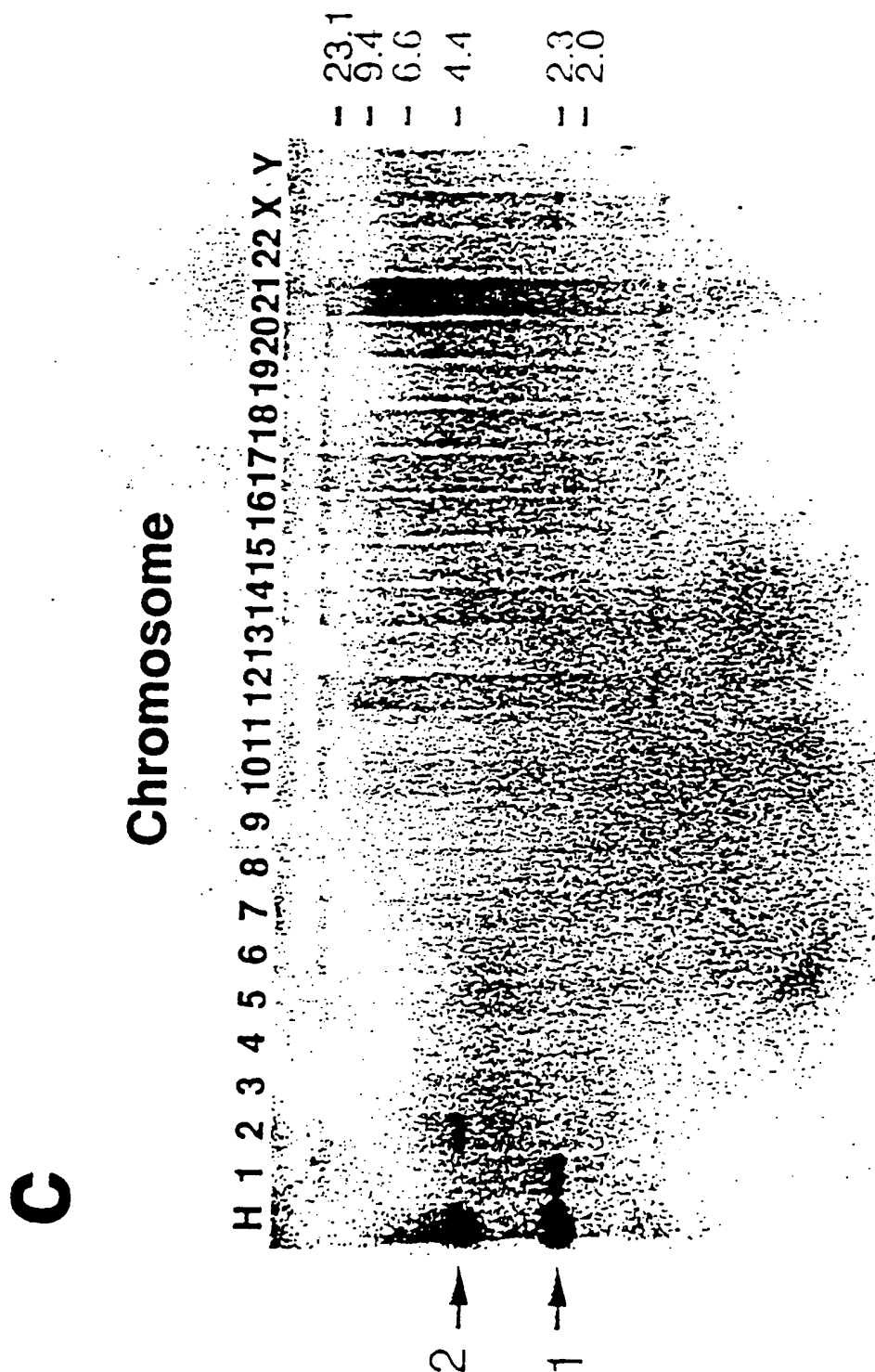


Fig. 19

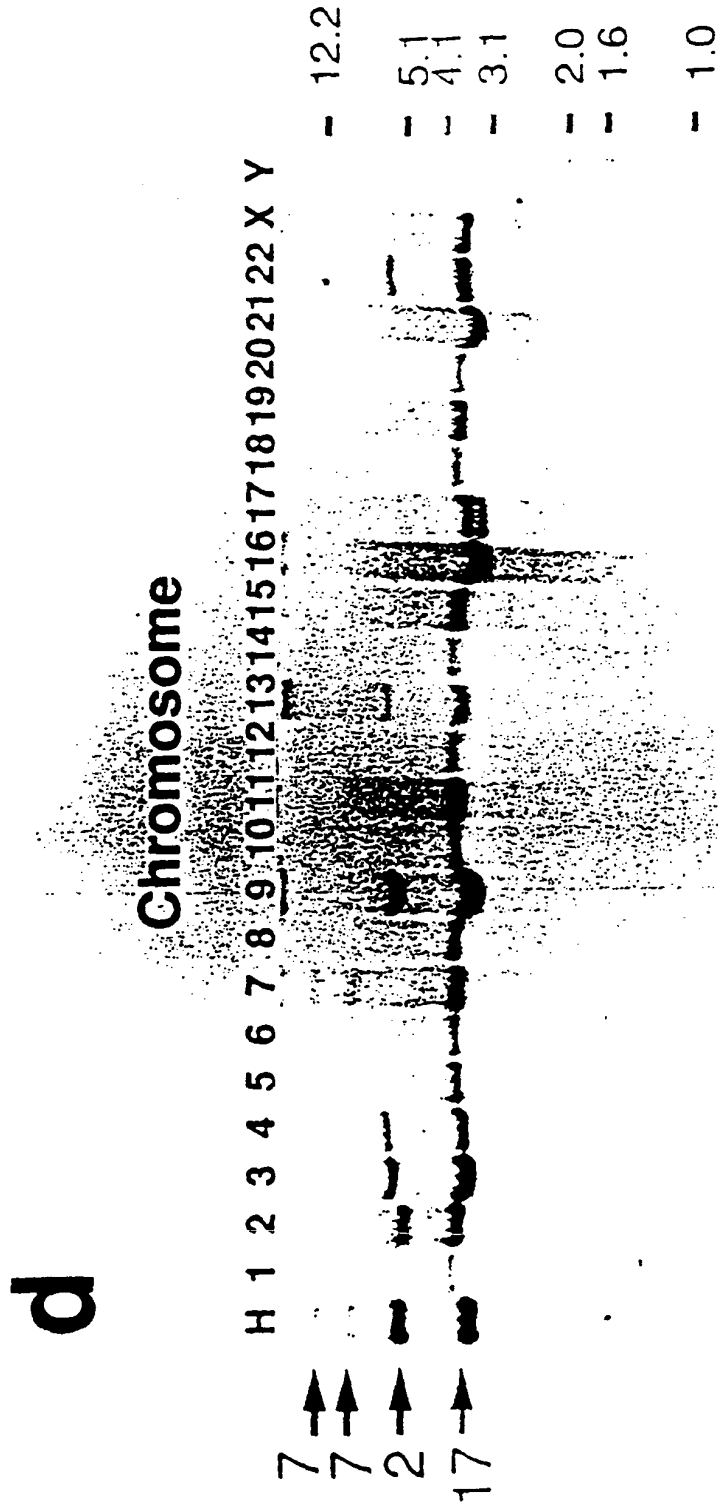
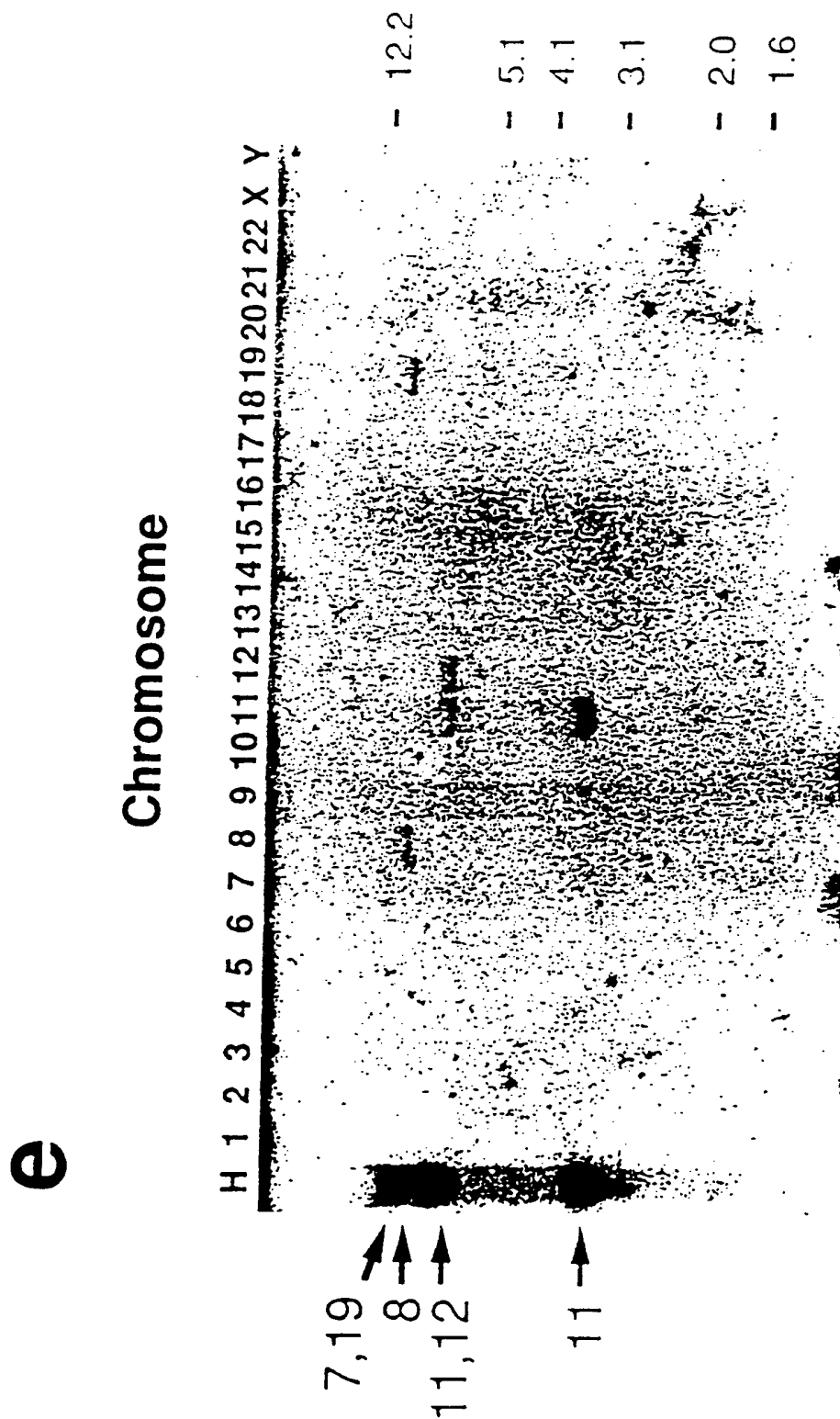


Fig. 20



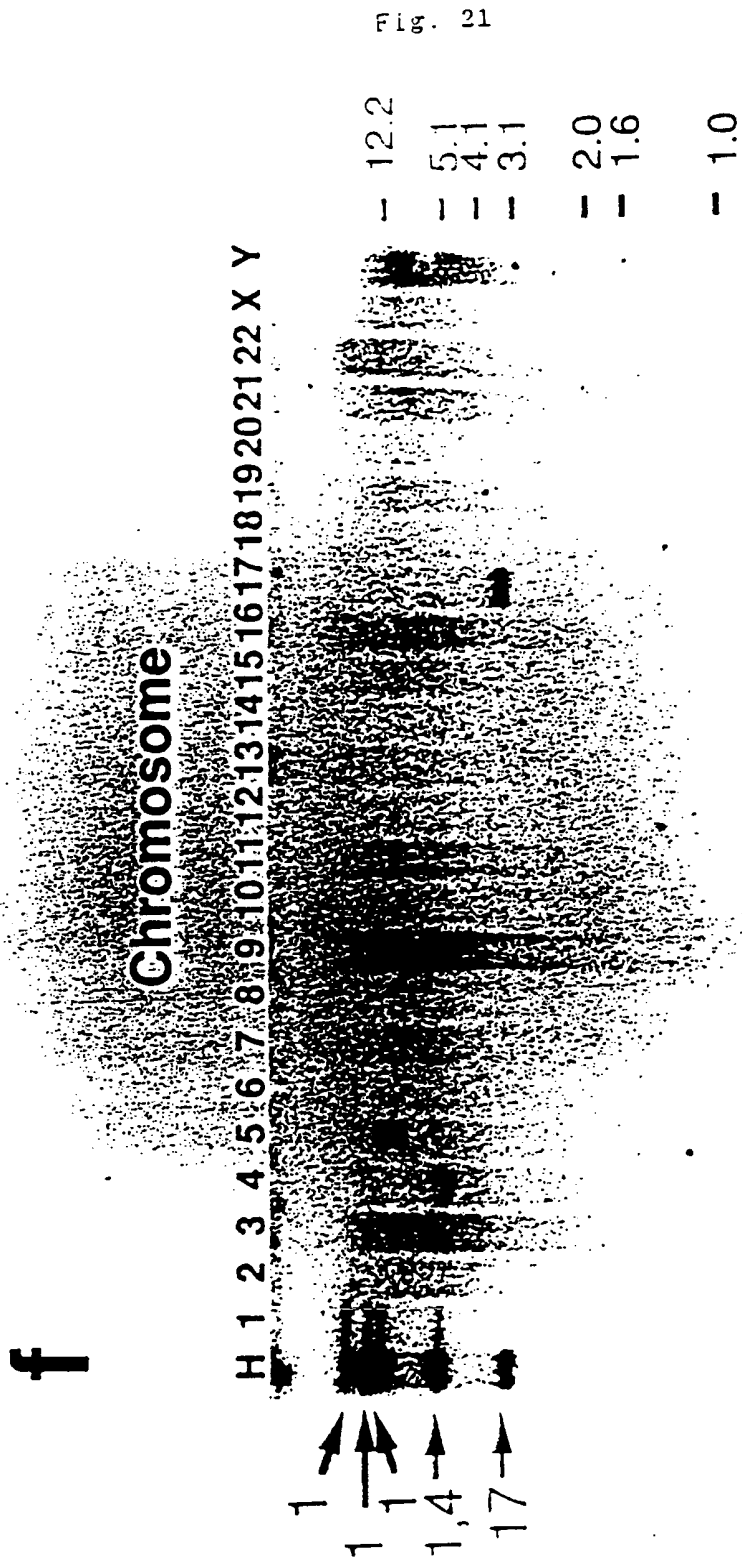


Fig. 21

Fig. 22

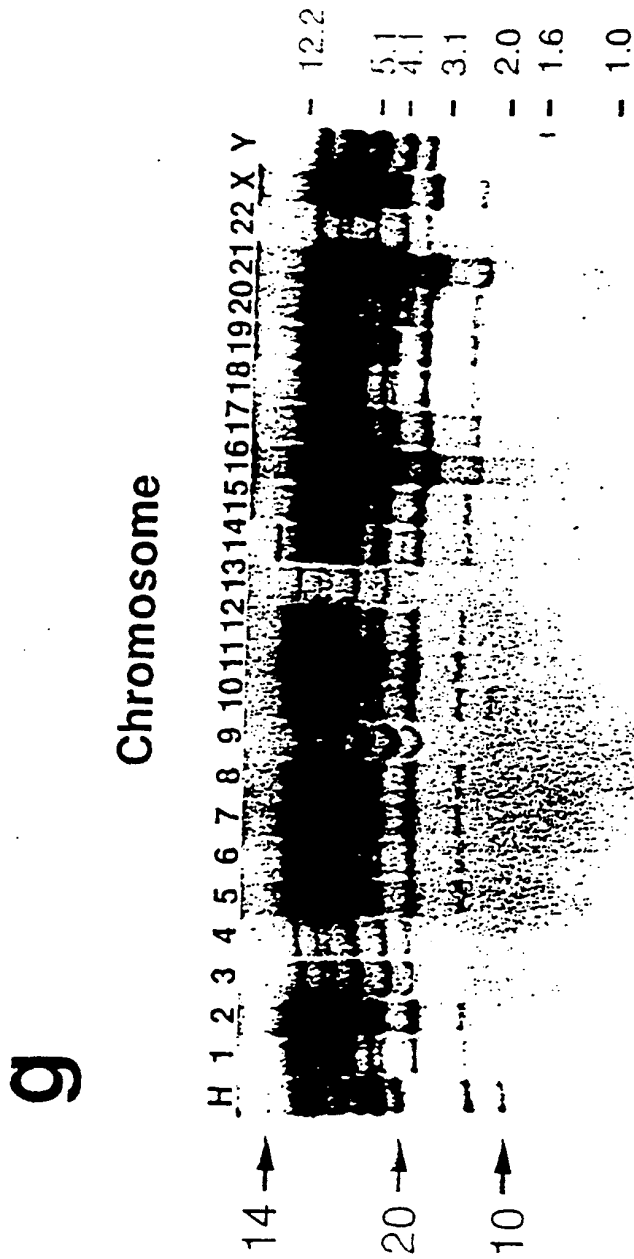


Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes				Chromosomes assigned		Background		
Clone	Sequence length	$\equiv$	$\equiv/3_1$	$\equiv/3_2$	$\equiv/3_3$	Mouse	Chinese hamster	
Single band group:								
cl2e11	GS000075	432	1	1	1	9	0	0
cl2e06	GS000062	540	1	1	1	6,15	0	0
cl2g01	GS000290	212	1	1	1	2	1	1
cl3e05	GS000117	359	1	1	1	11-	0	0
cl3e07	GS000120	355	1	1	1	2	0	0
cl3f10	GS000206	267	1	1	1	14	0	0
cl3h01	GS000279	133	1	1	1	12-	0	0
cl3h02	GS000322	167	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	3	0	0
d0h07	GS000154	313	1	1	1	11	1	1
d1b10	GS000348	153	1	1	1	20	0	0
hm01a12	GS000223	246	1	1	1	77	0	0
hm01c09	GS000423	157	0	1	1	1	0	0
hm01e12	junk	394	1	1	1	17	0	0
hm01f05	GS000066	434	1	1	1	19,22	0	0
hm01f10	GS000299	173	0	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	10	0	0
hm02e01	GS000203	271	1	1	1	16	0	0
hm02e01	GS000015	590	1	1	1	20	0	0
hm02e02	GS000342	156	0	1	1	14	0	0
hm02e05	GS000401	225	1	1	0	n.d.	0	0
hm02g02	GS000191	273	1	1	1	17	0	0
hm05a05	GS000251	219	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	0	0
kmd01	junk	169	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	5	0	0
s110	GS000057	471	1	1	1	3	0	0
s11d11	GS000307	#175	0	0	0	7	0	0
s11h01	GS000299	204	1	1	1	3	0	0
s147	GS000050	461	1	1	0	2	0	0
s14e06	junk	639	1	1	1	1	0	0
s14g02	GS000132	322	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	4	1	1
s150	GS000143	330	1	1	1	17	0	0
s156	GS000002	306	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	14	0	0
s179	GS000275	196	1	1	1	n.d.	0	0
s246	GS000234	241	1	1	1	9	0	0
s247	GS000347	153	1	1	1	1	0	0
s270	junk	135	1	1	1	19	0	0



Fig. 24

Numbers of bands detected with human whole chromosomes				Chromosomes assigned			Background		
Clone	Sequence length	E	E/B <sub>1</sub>	E/B <sub>2</sub>	B <sub>1</sub> /B <sub>2</sub>		Mouse	Chinese hamster	
s306	GS000255	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000295	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s445	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	241	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	537	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s650	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000029	537	1	1	1	1	3,7	0	0
tw1-19	GS000213	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	3	1	1
tw1-43	GS000098	173	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group:									
e12f12	GS000195	277	1	2	2	2	1,	1	1
e13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	5
hm01a07	GS000207	249	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000131	292	2	2	2	2	1,2	0	0
hm02a08	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	253	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm05f07	GS000043	503	1	1	2	1	3,	0	0
sl1d06	GS000268	205	2	2	2	2	11,12	0	0
sl1g12	GS000337	255	2	2	2	2	6,	0	0
sl124	GS000083	404	2	2	2	2	9,	1	1
sl144	GS000122	342	1	2	2	2	1,7	0	0
sl14f03	GS000239	243	1	2	2	2	2,	3	2
sl15c02	junk	439	2	2	1	2	6,	0	0
sl16b09	junk	420	1	1	1	2	10,14	0	0
sl17c09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	284	2	2	2	2	11,	0	0
s254	GS000124	353	2	2	2	2	1,	3	1
s255	GS000225	239	2	2	2	2	11,	0	0
s272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes				Chromosomes assigned				Background	
Clone	Sequence length	E	E/B <sub>1</sub>	E/B <sub>2</sub>	E/B <sub>3</sub>	E/B <sub>4</sub>		Mouse	Chinese hamster
s311	GS000092	133	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	GS000100	139	0	0	1	2	14,14	1	1
s336	GS000134	137	2	2	2	2	12,14	0	0
s333	GS000139	233	2	2	2	1	22,X	0	0
s339	GS000233	137	2	1	1	2	17.	0	0
s394	GS000063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GS000236	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s635	junk	250	1	1	1	2	9,13	0	0
s639	GS000297	205	1	2	2	2	2,X	0	0
s656	GS000025	#590	2	2	0	2	6,11	0	0
twl-33	junk	352	2	2	2	2	1.	0	0
twl-39	GS000153	#321	2	2	2	2	17.	0	0
twl-70	GS000061	441	1	1	2	1	11.	0	0
twl-80	junk	453	2	2	1	2	9,17	2	2
twl-87	GS000152	316	2	2	2	2	7.	0	0
Three band group									
d0h06	GS000030	417	3	3	3	1	1.	0	0
hm05b07	junk	336	2	3	3	3	5.	0	0
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s119	GS000107	373	3	3	3	3	n.d.	1	1
s173	GS000357	146	1	2	2	3	2.	0	0
s17a10	GS000294	181	3	3	3	3	2,13,22	1	1
s308	GS000412	638	2	2	2	3	X,X	1	1
s401	GS000224	249	2	3	3	3	6,6.	0	0
s654	GS000045	491	3	3	3	3	1,22.	0	0
twl-82	GS000208	267	3	3	3	3	13.	4	0
Four band group									
cl2g07	GS000154	320	4	4	2	3	5, 14.	0	0
cl3a08	GS000055	508	3	3	4	4	2,7,7,17	1	2
cl3c04	GS000106	#376	4	3	3	3	n.d.	0	2
cl3e09	GS000302	195	4	2	4	4	2,17.	7	2
s136	GS000160	515	4	4	4	4	4,X.	2	1
s163	GS000004	#618	4	4	4	2	4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
cl2f08	GS000253	217	5	5	5	2	2,7,9,14.	2	0
he01	junk	374	12	12	13	18	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
he10	junk	173	6	2	3	3	6,8,9,19,21.	3	3
hm01c05	GS000205	176	9	7	5	5	X	9	8
hm01f04	GS000246	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background		
Clone	Sequence length	E	E/3:	E/3:	3/3:		Mouse	Chinese hamster	
hm02f09	CS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	CS000096	171	5	6	4	6	2,3,17,	3	3
hm05a04	CS000236	#239	6	6	6	7	n.d.	8	5
kmb01	junk	350	5	5	5	5	13,	14	7
s11f06	CS000315	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3
s14f01	CS000407	262	12	11	10	9	1,5,9,13,	6	3
s173	CS000094	337	5	4	6	3	1,1,1,1,4,17	0	0
s255	CS000323	167	10	12	11	14	13,	9	5
s341	junk	494	9	9	8	6	n.d.	15	3
s406	CS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X,	3	5
tw1-63	junk	203	3	10	10	12	3,4,	17	11
Bands no detected:									
e13g02	CS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	CS000274	196	0	0	0	0	-	-	-
s323	CS000273	194	0	0	0	0	-	-	-
s359	CS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	CS000012	#734	0	0	0	0	-	-	-
s647	CS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

## A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA:coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)

☒ Further documents are listed in the continuation of Box C.☐ See patent family annex.

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"&amp;" document member of the same patent family

Date of the actual completion of the international search

February 6, 1995 (06. 02. 95)

Date of mailing of the international search report

March 7, 1995 (07. 03. 95)

Name and mailing address of the ISA/

Japanese Patent Office

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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
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X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
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X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

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International application No.

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
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X	Oncogene, Vol. 5, 1990, Firmbach-Kraft, I. et al. "Tyk 2, prototype of a novel class of non-receptor tyrosine Kinase genes" p. 1329-1336	1-6 (1345)
X	Science, Vol. 248, 1990, Smith, C. A. et al. "A receptor for human tumor necrosis factor defines an unusual family of cellular and viral proteins" p. 1019-1023	1-6 (1431)

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International application No.

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 263, 1988, Luster, A. D. et al. "Molecular and biochemical characterization of a novel gamma-interferon-inducible protein" p. 12036-12043	1-6 (1455)
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X	J. Cell Biol., Vol. 105, 1987, Argraves, W. S. et al. "Amino Acid Sequence of the Human Fibronectin Receptor" p. 1183-1190	1-6 (1607)
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X	EMBO J., Vol. 6, 1987, Willison, K. et al. "The human homologue of the mouse t-complex gene, TCP1, is located on chromosome 6 but is not near the HLA region" p. 1967-1974	1-6 (1749)
X	J. Biol. Chem., Vol. 266, 1991, Wu, Y. et al. "Activation of globin gene expression by cDNAs from induced K562 cells: Evidence for involvement of ferritin in globin gene expression" p. 17566-17572	1-6 (1785)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ikuta, T. et al. "Three human alcohol dehydrogenase subunits: cDNA structure and molecular and evolutionary divergence" p. 634-638	1-6 (1864)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Fukumoto, H. et al. "Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein" p. 5434-5438	1-6 (1878)

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International application No.

PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Clin. Invest., Vol. 76, 1985, Cooke, N.E. et al. "Serum vitamin D-binding protein is a third member of the albumin and alpha fetoprotein gene family" p. 2420-2424	1-6 (1888)
X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
X	J. Biol. Chem., Vol. 266, 1991, Huang, S.-H. et al. "Additions and corrections Human deoxytidine kinase. Sequence of cDNA clones and analysis of expression in cell lines with and without anzyme activity" p. 5353-5353	1-6 (1894)
X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al. "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
X	Gene, Vol. 44, 1986, Board, P. G. et al. "Molecular cloning and nucleotide sequence of human alpha-1 acid glycoprotein cDNA" p. 127-131	1-6 (1921)
X	Eur. J. Biochem., Vol. 155, 1986, Wathelet, M. et al. "Molecular cloning, full-length sequence and preliminary characterization of a 56-kDa protein induced by human interferons" p. 11-17	1-6 (2101)



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Biochemistry, Vol. 25, 1986, Koide, T. et al. "Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA" p. 2220-2225	1-6 (2174)
X	Biochemistry, Vol. 22, 1983, Friezner-Degen, S. J. et al. "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin" p. 2087-2097	1-6 (2214)
X	Biochem. J., Vol. 268, 1990, Steinkasserer, A. et al. "Heterogeneity in human serum amyloid A protein. Five different variants from one individual demonstrated by cDNA sequence analysis." p. 287-193	1-6 (2238)
X	Nucleic Acids Res., Vol. 17, 1989, Fabrizi, G. M. et al. "Sequence of a cDNA specifying subunit VIIa of human cytochrome c oxidase" p. 7107-7107	1-6 (2264)
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